Sequence

4X283559

AX659881 Sequence AF22589 Homo sapi AC125238 Homo sapi AC13799 Mus muscu AC110230 Mus muscu AC110339 Homo sapi AC098295 Rattus no AC102390 Wus muscu AC10231 Homo sapi AC053431 Homo sapi AC05874 Homo sapi AC05878 Rattus no AC12540 Rattus no AC12540 Rattus no AC127373 Mus muscu AC0513737 Mus muscu AC127373 Mus muscu AC05159 Homo sapi AC152069 Rattus no AC127373 Mus muscu AC127373 Rus muscu AC0516270 Rattus no AC127373 Mus muscu AC152069 Rattus no AC127373 Mus muscu AC152708 Hyporica BX54598 Zebrafish A63755 Sequence

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Run on:

Sequence:

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L PLEALT: JP 2002524081-A 8 06-AUG-2002;
SLOAN KETTERING INSTITUTE FOR CANCER RESEARCH
OS SYNCHACLIC CONSTINCT
PN JP 2002524081-A/8
PN 06-AUG-2002
PP 03-SEP-1999 UP 2000568998
PR 04-SEP-1999 UP 2000568998
PP 04-SEP-1999 US 60/0999138
PC C12N15/09, A61K35/26, A61K35/76, A61K39/395, A61K48/00, A61P35/00, PC C12N15/10//C07R16/44, C12N15/00, C12N5/10//C07R16/44, C12N15/00, CC C12N5/10//C07R16/44, C12N15/00, PC C12N5/00, P
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I tbases 1 to 30.
Sadelain, M., Bander, N.H. and Gong, M.
Fused receptor specific to prostate-specific membrane antigen and
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 30; Conservative 0; Mismatches 0; Indels
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JP 2002524081-A/8.
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AF344847 Papio cyn
AF344845 Callithri
AF344852 Macaca ne
AF344855 Macaca mu
AR102241 Sequence
BD267803 Methods a
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M37815 Human T-cel
AR102242 Sequence
AX557214 Sequence
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CQ715869 Sequence
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BD015187 TLiSa cel
J02988 Human T-cel
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                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                              1 tcgaggatcttgtcaggagcgataggctgc 30
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  nucleic search, using sw model
                                                                                                                                                              7, 2005, 10:58:39
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Minimum DB Maximum DB

Database

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DEFINITION

AE005756

RESULT

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ACCESSION

REFERENCE AUTHORS

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Ayllaayddukagrpprykprpstydberseaaftdlimenagldsgkppppprrdp
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APLI ATLPEGEAWTLLDA I REAQQDGEYDGR PRRWRSQPDLAARWPRLAVALSRTTQD
RFGRDADFYDSLMSLLGSDYRSNPELTLMLSGRSNDI I AWAERELVAPANLTASSVGP
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RFAAGSVWTDSDRQALAPAISAWDKRYANESNESWWQTDPAMRKAANGQPITAKDIMP
LKPVSCAS"
                                                                                                                                 'note="identified by match to protein family HMM"
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/note="identified by match to protein family HMM"
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protein id="AAK22787.1"
db_xref="GI:13422047"
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                                         complement (2112. .3659)
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'gene="CC0799"
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LFGANVRLPARGBELVTP"
LFGANVRLPARGBELVVTLLD
LFGANVRLPARGBELVVTLD
LFGANVRLPARGBELVVTLD
                                                                                                                                                                                                                                                                                                                 BCT 12-JUN-2002
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1 (bases i to 10951)

1 (bases i to 10951)

Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Bisen, J., Heidelberg, J.E., Alley, M.R., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Bly, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M.B., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J., Nierman, W.C., Feldblyum, T.V., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolff, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
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PID:1668766; identified by sequence similarity; putative"
/codon start=1
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/producT="sialic acid-specific 9-O-acetylesterase,
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Submitted (31-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
1. .10951
                                                                                                                                                                                                                                                                                                             AE005756 10951 bp DNA linear BCT 12-JUR
Caulobacter crescentus CB15 section 82 of 359 of the complete
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Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
21173698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:190650"
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Caulobacter crescentus CB15
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AE005756.1 GI:13422042
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177. .2102
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TITLE JOURNAL

TITLE JOURNAL MEDLINE

PUBMED REFERENCE AUTHORS

us-09-786-502a-8.rge

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GVLACYSLLVTVAFSIFCMRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY
RS'
2. .55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercocebus torquatus atys
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
                Direct Submission
Submitted (02-FEB-2001) Pathology and Laboratory Medicine, Emory
University School of Medicine, Winship Cancer Institute, 1365B
Clifton Rd, Atlanta, GA 30322, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning, sequencing, and homology analysis of nonhuman primate Fas/Pas-ligand and co-stimulatory molecules Immunogenetics 53 (4), 315-328 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-FBB-2001) Pathology and Laboratory Medicine, Emox University School of Medicine, Minship Cancer Institute, 1365B Clifton Rd, Atlanta, GA 30322, USA Location/Qualifiers
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Villinger.F., Bostik.P., Mayne,A., King,C.L., Genain,C.P.,
Weiss,W.R. and Ansari,A.A.
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    . 668
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                                                                                                                                                                                                                                                                                                               /note="co-stimulatory molecule"
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                                                                                                                                                                                /organism="Papio anubis"
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sub_species="anubis"
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2. .664
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AF344842.1 GI:13655470
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Villinger, F.
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  Villinger, F
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AF344842/c
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/ db xref="G1:13422049"

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/ translation="MTDWDSLDAGKYRDEAAVIADLLAAKPLSSEDRAAVRAEAEALV

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VGKLSNGAGPERAGHGVVGKLSALCPRYEATHEDRVWEELYPRTLALLAKTAARHNINFT

IDAEBADRLALSLKLLDKLCREPELGDWTGLAVQNYQKRGGERJALIAEALSEETGR

RLMVRLVKGAYWBASVTGVKIELDERVPVFTYKPATDLSVLVNAKALIEAAPHLYAQF

ATHNAHTLAAVVRMAKNTGVKIEHGRHGMGSPLYKAADDLVOGTTLARYAPVGGHED

LLPYLVRRLLENGANTSFVHALLDERVPVEKVVTDFIDTVEAHPDRHAKIPTIANVG

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PGRGETVGAALTSHEDLDGVAFTGGTDTAWRINQTLAARQGPIVPFIAETGGLNGMFV
DTTAQREQVIDDVIVSAFGSAGQRCSALRLLFLPHDTADHIIEGLKGAMDALVLGDPA
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REVFGPVLHVVRYKPENLEKVAGALAARRYGLTLGIHSRI ESFAADVQRLVPAGNAYV
NRSMTGAVVGVQPFGGEGLSGTGPKAGGPHALLRFAVERALSVNI TAQGGDPALLNL"
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF344837 16-SEP-20 ARNA linear PRI 06-SEP-20 Papio cynocephalus anubis CD28 protein precursor, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                'note="identified by match to PFAM protein family HMM
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Villinger,F., Bostik,P., Mayne,A., King,C.L., Genain,C.P.,
Weiss,W.R. and Ansari,A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="proline
dehydrogenase/delta-1-pyrroline-5-carboxylate
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                        'note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5229 TCCAGGATCTCGTCAGGATCGCTGGGCTG 5257
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                                                                                                                                                                                                                                                                                      complement (7610. .10699)
/gene="CC0804"
                                                                                                                                                                                                                                          complement (7610. .10699)
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Papio anubis
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/transl_table=11
                                                                                  table=11
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Gaps

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Length 668; 1; Indels PRI 06-SEP-2001

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GVLACYSLLVTVAFCIFWMRSKRSRLLHSDYMNMTPRRPGFTRKHYQPYAPPRDSAAY
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-FBB-2001) Pathology and Laboratory Medicine, Emory
University School of Medicine, Winship Cancer Institute, 1365B
Clifton Rd, Atlanta, GA 30322, USA
Location/Qualifiers
                                                                                                                                                   1 (bases 1 to 668)
Villinger, P., Bostik, P., Mayne, A., King, C.L., Genain, C.P.,
Willinger, P., Bostik, P., Mayne, A., Cloning, Sequencing, and homology analysis of nonhuman primate
Cloning, Sequencing, and homology analysis of nonhuman primate
Pas/Pas-ligand and co-stimulatory molecules
Immunogenetics 53 (4), 315-328 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="co-stimulatory molecule"
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/db_xref="taxon:9545"
2. ~664
                                                Macaca nemestrina (pig-tailed macaque)
              AF344852.1 GI:13655492
                                                                                                                                                                                                                                                                                                                2 (bases 1 to 668)
Villinger, F.
                                                                       Macaca nemestrina
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AF344855/c
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YVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWALVVVG
GVLACYSLLVTVAFRIFWMRSKRSRLLHSDYMMTPRRPGPTRKHYQFYAPPRDFAAY
RS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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NLFSRQPGASHKGVDSANGANGANGANGANGANGANG
VLASYSLLVTVALSVPWMRSRRSRLLHSDYNNMTPRCPGFTRRHYQPYAPPRDFAAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Callithrix jacchus (white-tufted-ear marmoset)
Callithrix jacchus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-PEB-2001) Pathology and Laboratory Medicine, Emory
University School of Medicine, Winship Cancer Institute, 1365B
Clifton Rd, Atlanta, GA 30322, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Callithrix.

1 (bases I to 668)

Villinger, F., Bostik, P., Mayne, A., King, C.L., Genain, C.P.,
Weiss, W.R. and Ansari, A.A.
Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules
Immunogenetics 53 (4), 315-328 (2001)
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Macaca nemestrina CD28 protein precursor, mRNA, complete cds.
AF344852
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                                                                                                         Score 20.4; DB 9; Length 668;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
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/organism="Callithrix jacchus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9483"
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                                                                                                                                                                                             CTTGTCAGGAGCGATAGGCTGC 30
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                                                                                                             ch 68.0%;
l Similarity 95.5%;
21; Conservative (
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Villinger, F.
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AF344852/c
LOCUS
DEFINITION
ACCESSION
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ACCESSION
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AF344845/c
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Bukaryowanta.

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

1 (bases 1 to 668)

Villinger,F., Bostik,P., Mayne,A., King,C.L., Genain,C.P.,

Weiss, W.R. and Ansari,A.A.

Fas/Fas-ligand and co-stimulatory molecules

Immunogenetics 53 (4), 315-328 (2001)

11491855
                                                                                                                                            Gaps
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Macaca mulatta CD28 protein precursor, mRNA, complete cds.
AF344855
AF344855.1 GI:13650007
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                                                                                                     Length 668;
                                                                                                                                            Indels
                                                                                               ch 68.0%; Score 20.4; DB 9; 1 Similarity 95.5%; Pred. No. 1.1e+02; 21; Conservative 0; Mismatches 1;
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Macaca mulatta
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us-09-786-502a-8.rge

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L Patent: JP 2002512203-A 6 23-APR-2002;
THE UNIVERSITY OF VERMONT AND STATE AGRICULTURAL COLLEGE
OS Homo sapiens (human)
PN JP 2002512203-A/6
PD 23-APR-1999 JP 200554356
PR 17-ARR-1999 US 60/082250,29-JUL-1998 US 60/094519 PR 24-SEP-1998 US 60/08250,29-JUL-1998 US 60/094519 PR PC AGRICULTURAL K NEWELL
PC AGIX39/395,AGIK31/519,AGIK31/55,AGIK31/704,AGIK31/7056,AGIK31/PC PC AGIX39/17,AGIX38/21,AGIK45/06,AGIP3/10,AGIP35/00,C12N15/00, PC AGIX38/17,AGIR38/21,AGIR45/06,AGIP3/10,AGIP35/00,C12N15/00, PC
                                                                                                                                                                                                                             BD267803 1514 bp DNA linear PAT 17-JUL-2003 Methods and products related to metabolic interactions in disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PP-1998 US 60/101580
MARTHA K NEWELL
A61K39/395, A61K31/519, A61K31/55, A61K31/704, A61K31/7056, A61K31/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A61K38/17, A61K38/21, A61K45/06, A61P3/10, A61P35/00, C12N15/00, PC
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Seed, B.D.Do.M.B., Allen, J., Aruffo, A., Camerini, D., Lauffer, L.D.,
Oquendo, C.P., Simmons, D., Stamenkovic, I. and Stengelin, S.D.
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1514)

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C01N33/574,
C A61K37/12, A61K37/66, C12N15/00
C Methods and products related to metabolic interactions disease
Tonation/Qualifiers
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Location/Qualifiers
                                  Length 875;
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                                                                     Indels
                                Score 20.4; DB 6;
Pred. No. 1.1e+02;
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107254
                                                                     0; Mismatches
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                                                                                                                                     868 CGTGTCAGGAGCGATAGGCTGC 847
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                                Query Match
Best Local Similarity 95.5%;
Matches 21; Conservative
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                                                                                                                                                                                                         /codon_start=1
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GVLACYSLLVTVAFSIFWMRSKRSRLLHSDYMNMTPRRPGPTRKHYQPCAPPRDFAAY
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                             Direct Submission
Submitted (02-FBB-2001) Pathology and Laboratory Medicine, Emor
University School of Medicine, Winship Cancer Institute, 1365B
Clifton Rd, Atlanta, GA 30322, USA
Location/Qualifiers
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Pred. No. 1.1e+02;
0; Mismatches 1;

    664
    note="co-stimulatory molecule"

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Feldhaus, A. Lawrence. and Jones, L. Ann.
                                                                                                                 /mol_type="unassigned DNA"
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Sequence 1 from patent US 6083751.
AR102241
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547
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2 (bases 1 to 668)
Villinger, F.
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/organism="Homo
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04-OCT-2000 JP 2000305557
13-JUL-1990 US 553759
BRIAN SEED, ALEAANDRO ARUFFO, MARTIN AMIOT
C12N15/09, C07K14/725, G01N33/53, C12N15/00
TLiSa cell surface antigen and CD27 cell surface antigen, and
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Seed, B., Aruffo, A. and Amiot, M.
TLisa cell surface antigen and CD27 cell surface antigen, and
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Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1316 19-AUG-2003,
Location/Qualifiers
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ThiSa cell surface antigen and CD27 cell surface antigen, and
utilization thereof.
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Patent: JP 2001157592-A 5 12-JUN-2001;
THE GENERAL HOSPITAL CORP
OS Homo sapiens (human)
PN JP 2001157592-A/5
                                                                                                                                                                                                                                                                                                               AR380771 1514 bp DNI
Sequence 1316 from patent US 6607879.
AR380771
Rapid immunoselection cloning method
Patent: EP 0330191-A2 11 30-AUG-1989;
Location/Qualifiers
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BD015187.1 GI:22555994
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Homo sapiens (human)
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Unclassified.
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NLERBEREADSAHKGLDSAVBVCVVYARYSQQLQVYSKTGFOLDGKLGRESVTFYLQNL
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GVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMSPTCS 15-JAN-1995
Human T-cell-specific homodimer surface protein CD28 mRNA, complete
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Draft entry and computer-readable sequence for [1] kindly provided by B.Seed, 11-AUG-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="T-cell-specific homodimer surface protein signal
peptide"
154. 759
/gene="CD28"
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Aruffo,A. and Seed,B.
Molecular cloning of a CD28 cDNA by a high-efficiency COS expression system
Proc. Natl. Acad. Sci. U.S.A. 84 (23), 8573-8577 (1987)
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/note="T-cell-specific homodimer surface protein
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J02988.1 GI:338444
T-cell-specific homodimer surface protein.
Homo sapiens (human)
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Best Local Similarity 95.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 1;
Location/Qualifiers
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/db_xref="G1:338445"
/db_xref="GDB:G00-118-765"
                                (100). .(759)
Location/Qualifiers
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                                                                                                             sapiens"
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join(M37812.1:761. .812,M37813.1:65. .130,M37813.1:383. .421,
M37814.1:127. .251,122. .250)
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                                                                     .
note="G00-118-761. .812,M37813.1:65. .421,M37814.1:127. .251,
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order(M371111:252. 1467,1. 1121)
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1 (bases 1 to 3585)
Feldhaus, A.Lawrence. and Jones, L. Ann.
Chimeric receptors for the generation of selectively-activatable TH-independent cytotoxic T cells
Patent: US 6083751-A 2 04-JUL-2000;
                 oin(M37812.1:539. .812,M37813.1:65. .421,M37814.1:127.
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llarity 95.5%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 1;
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Sequence 2 from patent US 6083751.
AR102242.1 GI:12813040
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join(M37812.1:539. .812,M37813.1:65. .421,M37814.1:127. .251,
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1 (bases 1 to 3230)

Lee,K.P., Taylor,C., Petryniak,B., Turka,L.A., June,C.H. and Thompson,C.B.

The genomic organization of the CD28 gene. Implications for the regulation of CD28 mRNA expression and heterogeneity

J. Immunol. 145 (1), 344-352 (1990)
                                                                                                                                                                                                                                                                                                                                                                                Chimeric receptors for the generation of selectively-activatable TH-independent cytocoxic T cells Patent: US 6083751-A 3 04-JUL-2000; Location/Qualifiers
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join(M37812.1:539. .984,M37813.1:1. .542,M37814.1:1.
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Length 1514;
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Human T-cell membrane glycoprotein CD28 mRNA, exon 4.
M37815
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ch 68.0%; Score 20.4; DB 9; Similarity 95.5%; Pred. No. 1.2e+02; 21; Conservative 0; Mismatches 1;
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Feldhaus, A. Lawrence and Jones, L. Ann.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
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                                                                                        766 CGTGTCAGGAGCGATAGGCTGC 745
                                                                     9 CTTGTCAGGAGCGATAGGCTGC 30
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glycoprotein CD28.
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PAT 03-FEB-2004

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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bluestone, J.A., Collins, M., Whitters, M., Griffin, M. and Kranz, D. Surface-bound antigen binding portions of antibodies that bind to ctla-4 and cd28 and uses therefor Patent: WO 0179300-A 3 25-OCT-2001; GENETICS INSTITUTE, INC. (US) Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 1803 from Patent WO02068579.
CQ715869
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     0; Mismatches
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Sequence 3 from Patent WO0179300.
AX283559 GI:17044297
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Location/Qualifiers
                                                         889 CGTGTCAGGAGCGATAGGCTGC 868
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Agents that specifically block cd28-mediated signaling and uses
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                                                                                                       68.0%; Score 20.4; DB 6; Length 3585; larity 95.5%; Pred. No. 1.3e+02; Conservative 0; Mismatches 1; Indels 0;
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Patent: WO 0300583-A 1509 30-JAN-2003;
Sagres Discovery (US)
Location/Qualifiers
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Sequence 1509 from Patent W003008583.
AX695882
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Genetics Institute, LLC (US)
Location/Qualifiers
Location/Qualifiers
1. .3585
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Sequence 1 from Patent WO02066059.
AX557214
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rpt family="MIR"
0439. .30783
note="L18270 Human chromosome 2 STS UT426"
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58600. .58721
/rpt_family="11"
complement(59586. .59701)
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/rpt family="Alu"
32555. .37857
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'Typt family='MER33"

Complement (5558..5834)

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5852..5898

/rpt_family='MER3"

complement (6534..6827)
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complement(8239, .Reforter)
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>406. .5550
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33985. .34281
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35580. .35863
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43887. 44156

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1610. .21890
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1 (bases I to 106539)

Fitzpatrick, B.S., Hammond, H.A., DeAngelis, D.M., Soderman, A.R., Wright, J.L., Liu, X., Larson, D., McGowan, J., Ziegler, S., Pritchard, L., Hess, J.F., Todd, J., Caskey, C.T. and Metzker, M.L. Buirect Submission
Submitted (18-JAN-2000) Department of Human Genetics, Merck & Co., Inc., SunneyTown Pike, West Point, PA 19486, USA
                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens PAC clone 219d7, complete sequence.
AF225899
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Novel compositions and methods for cancer
Patent: WO 03008583.A 1508 30-JAN-2003;
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                                                  Sequence 1508 from Patent W003008583.

    .51365
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3588. 3657
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3982. 4274
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Location/Qualifiers
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3214. .3294
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AC125238 196622 bp DNA linear PRI 15-OCT-2002
Homo sapiens BAC clone RP11-711C24 from 2, complete sequence.
AC125238
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Submitted (20-JUN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
M 63108, USA
4 (Dases 1 to 196622)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (08-AUG-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
S (Dases 1 to 196622)
Waterston,R.
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Submitted (16-AUG-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 196622)
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Submitted (15-OCT-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 16, 2002 this sequence version replaced gi:22138709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this ofone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 196622)
Sulston,J. B. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                Gaps
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Center code: WUGSC
                                                                                                                                              ;
                                                                                                          Length 106539;
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Nguyen,C., Bielicki,L. and Schatzkamer,K.
The sequence of Homo sapiens BAC clone RP11-711C24
Upublished (2001)
3 (bases 1 to 196622)
Waterston,R.H.
                                                                                                                                              Indels
                                                                                                        Query Match
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1;
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: H_NH0711C24
                                                                                                                                                                                                   69947 CGTGTCAGGACGATAGGCTGC 69926
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105891. .106161
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note="G09915 human STS CHLC.GGAA 19E07.P17317 clone
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                                                                                                                                                                        note="G06727 human STS WI-7843"
0776. .71041
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complement(102216. .102638)
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complement (92183. .92468)
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9944...7060c
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complement (62514. .63136)
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complement (68228. .68344)
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/rpt_family="Alu"
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omplement (93254. .93542)
rpt family="Alu"
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

donor, as described by Oscogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1.1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org The RPCI-11 human BAC library was made from the blood of one male

NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone. This clone is overlapped by AC069314 and AC010138.

A transposon was identified in the finished region of this clone and removed prior to submission. The transposon would insert after base pair 83916 of this sequence.

The sequence from base 156374 to base 156453 was derived from one plasmid subclone.

The sequence from base 156479 to base 156499 was derived from one plasmid subclone.

Polymorphisms have been identified between AC069314, AC010138 and this sequence.

Data from AC069314 and AC010138 was used to finish this clone.

Location/Qualifiers
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3296. 3599 rpt_family="Alu" /rpt_family="Alu" 2418. .2487 rpt_family="Alu" 'rpt_family="MIR" 1079. .2387 /rpt_family="Alu" /map="2' repeat_region FEATURES

68.0%; Score 20.4; DB 9; Length 196622;

Query Match

36123919	9263988	24493 F. family=	1655256	2575593 mr family-	599 56	62457	7525929	rpc_ramily= 0436552	rpt_ramily= 6706803	rpt_family= 8047097	98	/rpt_tamily="L2" 71937515	rpt 516		rpt 265	rpt. 566	rpt.	rpt_far	rpt_fal	rpt_fa	0773. rpt_fa	1076. rpt fa	1492	1927.	rpc_ramily="Mik" 214612237	rpt_ramily= 2238. 1253	1pc ramily="Alu" 253512682	rpt_family= 26831317	: tamily="MaLR" 7113193	rpc_ramily= 36211403	rpt_family= 46831496	rpt_ramily= 49671525	1530 1530	fpc_tamily= 57961607 rpt_family=	1607516315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkway, St. Louis, MO 63108, USA (bares 1 to 181025)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-NOV-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 181025)
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 18102s)
Shah,N. and Haglund,K.
The sequence of Mus musculus BAC clone RP23-444P22
Unpublished (2001)
                                                                                                                                                                     AC147243 181025 bp DNA linear ROD 06-FBB-
Mus musculus BAC clone RP23-444P22 from chromosome 6, complete
                      Gaps
                    ö
                 1; Indels
 95.5%; Pred. No. 2e+02; ive 0; Mismatches
                                                                         127308 CGTGTCAGGAGCGATAGGCTGC 127287
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ACI47243.2 GI:4135171
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. Similarity 95.5
21; Conservative
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The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone. This clone is overlapped by AC125175. 'rpt family="Ll"
10713 . 10767
'rpt family="ERV1"
1073 . 10775
10053 . 10175
10054 . 11097 6146..6348 /rpt_family="B2" 7452..7676 /rpt_family="MER1_type" 9087..9390 /rpt_family="MalR" 9643..9921 /rpt_family="L1" .181025
 /organism="Mus musculus" rpt_family="MER1_type" 13107. .13800 rpt_family="L1" 13794. .14072 /mol_type="genomic DNA /db_xref="taxon:10090" /chromosome="6" 19459. .19597 /rpt_family="RMER19B" 9600. .19894 rpt family="RMER19B" clone="RP23-444P22" clone_lib="RPCI-23" 1004. .1087 4/44 .4894 /rpt_family="Alu" 4224 .5110 /rpt_family="B2" 5236 .516 Location/Qualifiers 1004. .1087 /rpt_family="MIR" 2639. .3348 /rpt_family="L1" 3349. .4141 2349. .4141 /rpt_family="L1" 4744. .4894 /rpt_family="Alu" 11590. .11789 /rpt_family="L1" 11900. .12056 /rpt_family="B4" 5756. .500 5756. .5897 'rpt_family="Alu" /rpt_family="B4" 5449. .5610 'rpt_family="L1" 6735. .16861 /rpt_family="L1" 9459. .19597 /rpt_family="L1" 22270. .22768 /rpt_family="L1" 22777. .22848 .22848 /map="6 repeat_region source unsure FEATURES

/rpt_family="Alu"

Mapping information for this clone was provided by Dr. Wes Warren, obstrement of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

MAPPING INFORMATION:

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center: Washington University Genome Seguencing Center

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least come plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence; and the assembly was confirmed by restriction digest.

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AC123799 206894 bp DNA linear HTG 25-AUG-2002 Mus musculus chromosome UNK clone RP24-339P7, WORKING DRAFT SEQUENCE, 5 unordered pieces.
AC123799 AC123799 AC123799 HTGS_PRASE1; HTGS_PRASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (01-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

J. Chaese I to 208894)

Submitted (01-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

J. Chaese I to 208894)

Direct Submission

Submitted (125-AUG-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 206894) MCPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkway, St. Louis, MO 63108, USA
On Aug 8, 2002 this sequence version replaced gi:21307491
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Consensus quality: 205678 bases at least Q40
Consensus quality: 2056025 bases at least Q30
Consensus quality: 206025 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 206494; suum-of-contigs
Quality coverage: 19.54 in Q20 bases; sum-of-contigs
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0662 10761: gap of unknown length
0762 27598: contig of 16877 bp in length
1599 4768: gap of unknown length
1769 47568: gap of unknown length
1769 9754: contig of 19770 bp in length
1769 9754: contig of 50386 bp in length
1755 9764: contig of 108840 bp in length
1755 206894: contig of 108840 bp in length
1756 106814: contig of 108840 bp in length
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Contact: submissions@watson.wustl.edu
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39765. 40142
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source

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6 GATCTTGTCAGGAGCGATAGGCTGC 30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC110230 216521 bp DNA linear ROD 23-MAR-2
Mus musculus chromosome 6, clone RP23-54L18, complete sequence.
AC110230
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Mus musculus chromosome 6, clone RP23-54L18
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clone="RP24-339P7"
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Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,
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Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
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Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Suhmitted, V. V., M., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
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Submitted (11-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Brickeon, J., Faro, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illey, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Indblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Marchen, C., McCarthy, M., Meddrain, J., Mencus, L., Minova, T., Marthews, C., McCarthy, M., Meldrim, J., Mencus, L., Minova, T., Menga, V., Murphy, T., Naylor, J., O'Neull, D., Ollver, J., Peterson, K., Feura, R., Seamen, S., Schupack, R., Seamen, S., Severy, P., Roman, J., Schauer, S., Schupack, R., Seamen, S., Severy, P., Spencer, B., Stange-Thomann, V., Stojanovic, N., Stubes, M., Valanas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasailiev, H., Venkataraman, V.S., Viel, R., Vo, M., Viel, M., Vi
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Contact: sequence submissions@genome.wi.mit.edu
------- Project Information
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complement (1128. .1255)

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rpt_family="Lx"
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rpt family="L1 MM"
complement (8208. .8349)
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                                                                                                                                                      019. .6218
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 142422)
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Submitted (05-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 142422)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                        ACI13935 142422 bp DNA linear PRI 22-MAY
Homo sapiens chromosome 1 clone RP4-706A16, complete sequence.
ACI13935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and
                                                                                                                                   Length 216521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: Chr.1

Center clone name: RP4.706A16 (8c0534)

Sequencing vector: plasmid; 100% of reads Chemistry: Dye-terminator ET; 53% of reads Chemistry: Dye-terminator ET; 53% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 142421 bases at least Q40

Consensus quality: 142421 bases at least Q30

Consensus quality: 142422 bases at least Q20
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                                                                                                                                 Score 20.2; DB 10;
Pred. No. 2.5e+02;
0; Mismatches 3;
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25715. .26058
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complement (23503. . /rpt_family="L1_MM" 25401. .25714
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                                                                                                                                     Query Match 67.3%;
Best Local Similarity 88.0%;
Matches 22; Conservative (
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Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.	Sequence validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and	vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are on significant remaining discrepancies between the experimental and predicted values. Uniquely ordered	yy daghed lines. Bglii		3338 3384 11257 11189 3005 3039 	<800 10817 11189 8065	2814 2859 659 6800 486 6800 1247 1216 5351 5311 106 6800	4677 3324 3320 4	3373 3384 1771 1862 184 <800 2620 2688 293 <800 1815 1788	1870 . 1913	5137 1876 1862 994	6417 6365 1363 1323 1101 1107 939 950 90 <800 593 <800	7516	301 <800 1438 1425 3233 3251 1932 1913 4283 4295 6425 6475	5541 2805 2882 489	6755 6842 749 760 3031 3039 	<pre><800</pre>

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                                                                                                                                                                                                                                                                                                                                              AC098295 158498 bp DNA linear HTG 13-NOV-2002 Rattus norvegicus clone CH230-1113, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
                                                                       Gapa
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Query Match
66.7%; Score 20; DB 9; Length 142422;
Best Local Similarity 82.1%; Pred. No. 3e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0
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                                                                                                                                                               111649 TTGTGGATCTTGTGAGGAGTGATTGGCT 111622
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Worley, K.C.
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Direct Submission

Lountted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:23269254.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-geaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 148768 bases at least Q40
Consensus quality: 150137 bases at least Q30
Consensus quality: 151228 bases at least Q30
Estimated insert size: 150789; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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61352 61451: gap of unknown length
61452 155218: contig of 91067 bp in length
152519 152618: gap of unknown length
152619 158498: contig of 5880 bp in length.
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/db xref="taxon:10116"
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54598. .56029
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60299. .61351
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51452. .63331
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48957. .149957
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:50790. .152518
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/note="wgs_contig"
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57818. .60042
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SOURCE

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PRI 24-JUL-2002
                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBN
Web site: http://www-seq.wi.mit.edu
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Center clone name: 462 I 5
Center clone vector: Plasmid: n/a; 100% of reads
Sequencing vector: Plasmid: n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 16239 bases at least Q30
Consensus quality: 162714 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 162891; sum-of-contigs
Quality coverage: 11.9 in Q20 bases; sum-of-contigs
Quality coverage: 11.5 in Q20 bases; sum-of-contigs
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                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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/clone_lib="RPCI-24 Male Mouse BAC"
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/note="assembly_fragment"
8966. .28315
/note="assembly_fragment"
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vector_side:left"
5037. .5658
/note="assembly_fragment"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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S. (bases 1 to 16129).

Anderson, S., Barna, N., Bastlen, V., Boguslavkly, L., Boukhgalter, B., Anderson, S., Barna, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Haaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lewcoque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Matheri, D., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Connor, T., O'Donnell, P., O'Lawc, J., Peterson, K., Phuhkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wwan, D., Ye, W.J., Young, G., Lainer, M., Laine, M., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Phinish, M., Marker, M., Submer, A., Zalmer, A., and Zody, M., Submiss, M., Submer, M., Zambek, L., Zimmer, A., and Zody, M., Wan, Young, G., Phinish, M., Marker, M., Wan, W., Wan, W., Wan, W., Wan, W., Wa
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Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 163291)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chospi, T.,

Collymore, A., Cook, A., Cook, P., Corum, B., DeArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B.,

Direct Submission, Stanbar, M., Samba, M., Simber, A. and Zody, M.
                                                                                                                                                                                                                                                                               AC102390 163291 bp DNA linear HTG 07-JUN-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
I (bases 1 to 163291)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-46215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC102390.3 GI:31455734
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
97252 CTAGGATTCTGTCAAGAGGGATAGGCTG 97225
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TITLE
JOURNAL
REFERENCE
AUTHORS
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Gaps

COMMENT

DEFINITION ACCESSION VERSION KEYWORDS	Homo sapiens chromosome 1 clone RP11-363H12, complete sequence. AC093433 AL390781 AC093433.2 GI:21954025
SOURCE	sapie sapie ryota;
REFERENCE AUTHORS	on, M.V., Zhou, Y., C., Phelps, K.A.
TITLE JOURNAL REFERENCE	2613)
TITLE	<pre>Kaul, k.k., Olson, M.V., Kaymond, C., Clendenning, J., Ivey, R.G. and Haugen, B.D. Direct Submission Submitted (23-200-2001) Genome Center University of Washington</pre>
REFERENCE AUTHORS	98195, USA Zhou, Y., James, R.A., Rouse, G., Ds. K.A., Buckley, D., Kibukawa.
TITLE JOURNAL	002) Genome Center, University of Wash
COMMENT	BOX 32145, Seattle, WA 98195, USA On Jul 24, 2002 this sequence version replaced gi:15281284.
	Context University of Washington Genome Center
	Center Code: UM-C Web site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu
	Drafting Center: SC Project Information
	Center project name: chr-1 Center clone name: RP11-363H12 (sc0369)
	Sequencing vector: plasmid; L08752; 100% of reads
	Chemistry: Dye-terminator ET; 89% of reads Chemistry: Dye-terminator Big Dye; 11% of reads
	Assembly program: Phrap; version 0.990319 Consensus quality: 172300 bases at least Q40
	Consensus quality: 172573 bases at least Q30 Consensus quality: 172605 bases at least Q20
	insert size: 1/2613; sum-or-contigs Quality coverage: 10.0x in Q20 bases; sum-of-contigs
	Overlapping Sequences: 5': RP4-706A16 (UMGC:sc0534) AC113935, 49862-bp overlap 3': RP11-375A5 (UWGC:sc0306) AC095030, 1917-bp overlap
	Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than
	1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest

fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII HIGHIEL SeqDerMap FngrPrnt <800 <800 <800 <800 <800 <800 FngrPrnt **<800** <800 <800 <800 <800 SeqDerMap <800 <800 <800 <800 FngrPrnt SeqDerMap

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 17395) AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E. TITLE Homo sapiens chromosome 1, clone RP11-295E21	A O t	AUTHOKS BITTER, b. Intron, b., NuBbaum, c., Lauthet, p., Autaum, n., Allen, N., Anderson, S., Badwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,	Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Cooke, P., DeArellano, K., Dewar, Y., Diaz, J.S., J., Cooke, Domino M. Dovie M. Retreita D. Fitzlinch W. Gage, D.	Galagan, J., Gardyna, S., Glade, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Guarde, S., Goyette, M., Graham, L., Gand, Brown N. Grant G. Wanne B. Haaford B. Horton L.	Grand-Freie,N., Grand,G., nagus,D., nearly,A., nocaco,F., Howland,J.C., Iliev,I., Johnson,R., Johnson,C., Kann,L., Karatas,A., Vlein I Laboomie V Lamanares B Landers T Lebocky,J.	Alexin, u., inten,c., ind.c., nocke,K., mardonald,P., Marduis,N., Moforth, M. Mofora D. Moforth, M. Moforth D.	Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Mirova, T., O'Connor, T., O'Donnell, P.,	O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Diani, C. Pollara, V. Raymond, C. Rilev, R. Rodov, P., Rothman, D.,	Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,	Testaye,S., TheodoryJ., Tirrell,A., Travers,M., Triglio,J.,		JOURNAL Submitted (9-JUN-2000) Whitehead Institute/MIT Center for Genome JOURNAL School 200 Genome	COMMENT On Jun 25, 2000 this sequence version replaced gi:8347970.	All repeats were identified using Repeatmasker: Smit, A.F.A. & Green, P. (1996-1997)	nttp://ltp.genome.wasnington.edu/kw/kepeatwasker.ntml	Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR	Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu	Center project Information Conter project name: L10424	Centrel Cloud manner 200 = 21 Summary Statistics	Chemistry: Dye-terminator Big Dye; 100% of reads	Consensor quality: 159186 bases at least 040	Consequence quality: 10.430 Dases at least Q20	Quality coverage: 3.7 in Q20 bases; sum-of-contigs	* NOTE: This is a 'working draft' sequence. It currently * consists of 25 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as	* runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will	preserved. 1 1530: contig of 1530 bp in 1531 1630: gap of 100 bp	3100: contig 4696: contig 4796: gap of 6486: contig 6486: contig 8765: contig 1668: gap of	11168: gap of 100 bp
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6310	3039	6310 4569	993	<800	2464	<800	4050	<800	4569	10313	3039	2695	<800	2031	8985	774	2168	2464						Gaps	,		HTG 25-JUN-2000 WORKING DRAFT	
6218	2966	6218 4556	1009	601	2390	242	3947	392	4745	10356	3067	2680	189	1957	8983	160	2167	2461	; ; ; ; ; ;					Length 172613; ; Indels 0;			ьť	
1764	1266	1266	4844	<800	6629	1624	<800	3252	5389	1947	1764	1110	13359	4985	2191	<800	3858	847	5601	3858	<800	<800		9; e+02;	,	15	DNA 11-295E21	
1758	1282	1294	4788	325	6588	1639	107	3179	5478	1972	1754	1132	13764	4946	2124	644	3808	861	5569	3926	368	216	lifiers	20. No.		FGATTGGCT 19051	AC073027 Homo sapiens chromosome 1 clone RP11-295E21 map SEQUENCE, 25 unordered pieces. AC073027.2 GI:8705069 HTG; HTGS_PHASE1; HTGS_DRAFT.	
5986 9798	4009	1224	<800	1893	6812	1547	2208	<800	7711	2208	1441	859	1547	4335	<800								Location/Qualifiers	66.7%; 82.1%; ative	TGTCAGGAG	TGTGAGGAC	chromosc unordere GI:870506	(numan)
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16259 contig of 4685 bp in length 16259 gap of 100 bp 16359 and 100 bp 16359 and 100 bp 16359 and 100 bp 16359 and 16350 and 1
contig of 2629 bp in length
gap of 100 bp
contig of 2201 bp in length
gap of 100 bp
contig of 1976 bp in length
gap of 100 bp
contig of 2528 bp in length
gap of 100 bp
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contig of 2057 bp in length
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contig of 2214 bp in length
gap of 100 bp
contig of 3791 bp in length
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1. .1530
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ACU26874 203812 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 1 clone RP11-627E4, WORKING DRAFT SEQUENCE,
32 unordered pieces.
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Waterston, M. H.
Direct Submission
Submitted (24-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MN 63108, USA
On Sep 1, 2000 this sequence version replaced gi:7631093.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 203812)
Waterston, R.H.
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95927. .110448
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110549. .129502
/note="assembly_fragment"
129603. .151126
/note="assembly_fragment"
151227. .173995
/note="assembly_fragment"
                                                             /note="assembly_fragment"
4158. 49800
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49901. 57333
/note="assembly_fragment"
                                                                                                                                                                               57494. ..66985
/note="assembly_fragment"
67086. .82213
/note="assembly_fragment"
82314. .95826
/note="assembly_fragment"
31574. .36258
/note="assembly_fragment"
36359. .41057
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AC026874.4 GI:9958302
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOmo sapiens (human)
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9668 200798: contig of 2131 bp in length

9799 202089: gap of unknown length

1889 202307: contig of 1409 bp in length

1880 202407: gap of unknown length

1880 203812: contig of 1405 bp in length

1880 203812: contig of 1405 bp in length.

1880 203812: contig of 1405 bp in length.
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87014. .94398
/note="assembly_name:Contig26"
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16237. 178058
/note="assembly_name:Contig34"
178159. 195531
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196845. 198567
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                                                                                                                                                                                                                                                                                                                                                                      'note="assembly_name:Contig10"
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23781. .28919
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.04240. .113608
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                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
     Consensus quality: 190766 bases at least Q30 Consensus quality: 192884 bases at least Q20 Insert size: 192000; agarose-fp Insert size: 200712; sum-of-contigs Quality coverage: 3.83 in Q20 bases; agarose-fp Quality coverage: 3.83 in Q20 bases; sum-of-contigs
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contig of 17313 bp in length
gap of unknown length
contig of 1113 bp in length
gap of unknown length
contig of 1723 bp in length
gap of unknown length
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Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC115240 232735 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-153F4, WORKING DRAFT SEQUENCE, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                66.7%; Score 20; DB 2; Length 203812; 82.1%; Pred. No. 3.2e+02; ive 0; Mismatches 5; Indels 0;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                    86013 TTGTGGATCTTGTGAGGAGTGATTGGCT 85986
                                                                                                                                                                                                                                                                           1 TCGAGGATCTTGTCAGGAGCGATAGGCT 28
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Matches 23; Conservative
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                                  misc_feature
                                                                                                                                                          Query Match
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AC115240
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REFERENCE

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Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23101356.

The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.rec.edu/projects/ratl/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                        Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (Dases 1 to 232735) Rat Genome Sequencing Consortium.
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhusern, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
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152238 152337: gap of unknown length
152338 232735: contig of 80398 bp in length.
Location/Qualifiers
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Center code: BCM
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clone_end:Sp6
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Starty, D. Marie., MetAts)

Starty, D. Marie., MetAts)

Allan, C., Allan, H., Alsbrooks S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Bader, H., Bader, H., Badadaranalke, D., Barber, M., Barnstead, M., Benahmed, P., Blawalo, K., Blat, J., Blankenburg, K., Blyth, P., Brown, M., Braaken, J., Brishenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, G., Dereil, M., Derein, K., Duval, K., Duval, K., Duval, M., Davyak, K., Derein, K., Durah, M., Duron, K., Duval, M., Duron, K., Duval, M., Duron, M., Davon, K., Duron, M., Duron, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evane, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganter, M., Garza, M., Gebregeorgis, E., Geek, Gill, R., Garda, M., Garza, M., Gebregeorgis, E., Gesk, Gill, R., Garda, M., Hand, K., Duval, M., Hands, S., Hadan, S., Hander, S., Hadan, C., Hamilton, C., Hamilton, C., Hamilton, K., Harvalak, P., Hawes, A., Haddun, S., Hung, S., Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC120701 237445 bp DNA linear HTG 21-SEP-2002 Rattus norvegicus clone CH230-65H6, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                              ch 66.7%; Score 20; DB 2; Length 232735; 1. Similarity 82.1%; Pred. No. 3.2e+02; 23; Conservative 0; Mismatches 5. Tadala a
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                                                                                                                                                                                                                                                                                                                                                                                          218720 CTAGGATTCTGTCAAGAGGGATAGGCTG 218747
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end_sequence:BH336181"
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               228890. .230652
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230703. .232735
                                                                                                                        /note="wgs_contig"
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                                                                                         misc feature
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Direct Submission
Unpublished
2 (bases 1 to 237445)
2 (bases 1 to 237445)
2 (bases 1 to 237445)
3 (bases 1 to 237445)
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237445)
Rat Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237445)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 77 77030, USA On Sep 21, 2002 this sequence version replaced gi:21908396. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Betimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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867 233966: gap of unknown length
967 235011: contig of 1045 bp in length
012 235111: gap of unknown length
112 236137: contig of 1026 bp in length
138 2356237: gap of unknown length
138 237445: contig of 1208 bp in length
Location/Qualifiers
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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/note="clone boundary
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Standy, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alsbrooks, S., Amin, A., Anguiano, D., Anyalabehni, V., Aoyagia, N., Aoyagia, N., Anguiano, D., Anyalabehni, V., Aoyagia, N., Aoyagia, N., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baras, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baras, E., Chen, G., Carder, K., Cavazos, I., Cener, H., Cener, A., Cher, G., Carder, M., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheo, G., Corden, M., Chen, G., Dencon, S., Derano, C., Day, Carroll, L., De Anda, C., Dederich, D., Dayagado, O., Denson, S., Derano, C., Ding, Y., Dinh, H., Divya, K., Dederich, D., Dayagado, O., Denson, S., Derano, C., Ding, Y., Dinh, H., Divya, K., Bagan, A., Begene, C., Evane, C. R., Falls, T., Falls, M., Bagene, C., Evane, C. A., Falls, T., Falls, T., Farnier, M., Bagen, R., Chan, S., Mang, M., Guerra, M., Garza, M., Gebregoergis, E., Geer, K., Gill, R., Gardy, M., Guerra, M., Garza, M., Gebregoergis, E., Geer, K., Gill, R., Gardy, M., Guerra, M., Garza, M., Gebregoergis, E., Geer, K., Gill, R., Gardy, M., Guerra, M., Garza, M., Harlas, S., Haladma, S., Hande, S., Hongues, M., Hanli, C., Hamilton, C., Hamilton, C., Hamilton, Kovar, C., Liu, J., Lau, M., Lau, M., Hanli, S., Hunde, M., Manner, M., Martin, R., Mayan, M., Martin, R., Mayan, P., Martin, R., Mayan, M., Martin, R., Mayan, M., Martin, R., Reitly, M., Reitly, R., Reitly, M., Reitly, R., Savery, G
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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complement(222953. .233569)
/note="clone_boundary
clone end:Sp6
site:EcoRI
end_sequence:BH350815"
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Matches 23; Conservative
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SOURCE
ORGANISM
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RESULT 35 AC129059 LOCUS

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ACCESSION

REFERENCE AUTHORS

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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23264545.

The sequence in this assembly is a combination of BAC based reads and whole genome shockun sequencing reads assembled using Atlas (http://www.ngsc.bcm.tmc.edu/projects/rat/). Each conrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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* NOTE: This sequence may represent more than one clone.

* NOTE: This sequence may represent more than one clone.

* NOTE: This sequence may represent more than one clone.

* NOTE: This sequence may represent more than one clone.

* NOTE: This sequence may represent more than one clone.

* Consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warg, Q., Warg, S., Warren, T., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, Y., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 242268: contig of 242268 bp in length
242269 242368: gap of unknown length
242369 243439: contig of 1071 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 243439)
Rat Genome Sequencing Consortium.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                Unpublished
2 (bases 1 to 243439)
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Direct Submission
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300050 bp DNA linear BCT 17-MAY-2003
AP004596 BA000028
AP004596.1 GI:22776527
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Oceanobacillus iheyensis gen. nov., sp. nov., a deep-sea extremely
halotolerant and alkaliphilic species isolated from a depth of 1050
m on the Iheya Ridge
TEMS Microbiol. Lett. 205 (2), 291-297 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oceanobacillus iheyensis HTE811
Oceanobacillus iheyensis HTE811
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 66.7%; Score 20; DB 2; Length 280288; Similarity 82.1%; Pred. No. 3.3e+02; 23; Conservative 0; Mismatches 5; Indels 0
                       37815: cortig of 33153 bp in length 66758: contig of 28843 bp in length 66858: gap of unknown length 66858: gap of unknown length 99552: contig of 28674 bp in length 141609: contig of 41777 bp in length 141509: gap of unknown length 141509: gap of unknown length 200544: contig of 58935 bp in length 200544: contig of 58935 bp in length 200541: contig of 70127 bp in length 27477: contig of 70127 bp in length 27472: contig of 3701 bp in length 27472: contig of 2233 bp in length 276505: contig of 2233 bp in length 276505: contig of 2233 bp in length 276505: contig of 23383 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP23-42M8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66859. .99532
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Best Local Similarity
                                                                   37916
66759
66859
99533
141410
141510
200445
200445
270772
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276806
276906
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DEFINITION
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AP004596
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MEDLINE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus Microse mouse,

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

I (bases 1 to 280288)

McPherson, J.D. and Waterston, R.H.

Direct Submission

Submitted (14-JUJ.-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

Barkway, St. Louis, MO 63108, USA

Submitted (14-JUJ.-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park Direct Submission

Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC127373

280288 bp DNA linear HTG 25-AUG-2002
Mus musculus chromosome UNK clone RP23-42M8, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                      Query Match
66.7%; Score 20; DB 2; Length 243439;
Best Local Similarity 82.1%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0, 990319
Consensus quality: 277848 bases at least Q40
Consensus quality: 2777488 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC127373
AC1277373.1 GI:21747787
HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                        237133 daddarcerericaccaccreaccrec 237160
                                       complement (240371, .241219)
/note="clone boundary
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                                                                                                                                                                                                                                                                                                              3 GAGGATCTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- Genome Center
                                                                                                                                                         end_sequence:BH329263"
clone_end:T7
site:EcoRI
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                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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AUTHORS
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JOURNAL
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AUTHORS
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Gaps .; 0

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complement (2863. .3459)

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4496. .5290
4496. .5290
4496. .5290

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complement (2863. .3459)
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RVLQTNRNRYSLLELGLETGRKNQIRVHMEELGHPVVGDKRYGSKGRSVIGRLGLHAKI
LSFYHPVTNKLMLFRSDVPNAFFQKTK"

COMPLEMENT (1804. . 2799)
                                                    Takami,H., Takaki,Y. and Uchiyama,I.
Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MATISKGENKFYVGEDIRNPQAEITFVESGENRLVIDHTYVATD
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TTHFEQVEKYKKMIEEYLQEPIPEDLDVKDED"
                                                                                                                                                                                                                            Takami, H., Takaki, Y. and Chee, G.

Takami, H., Takaki, Y. and Chee, G.

Direct Submission

Direct Submission

Submitted (36-DEC-2001) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorgaisms Research Group; 2-15

Natsushima-cho, Yokosuka, Kanagawa 237-0061, Japan

(B-mail:takamih@jamstec.go.jp,

URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,

Tel:81-468-67-9643, Fax:81-468-67-9645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oceanobacillus iheyensis HTE831"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="OBO847"

/note="CDS_ID OBO847"

/codon start=1
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/transI_table=11
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/note="halotolerant and alkaliphilic"
154. .441
                                                                                                                                                     Nucleic Acids Res. 30 (18), 3927-3935 (2002)
22220767
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775. .1686
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                          REFERENCE
AUTHORS
TITLE
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Center project name: bA619A13
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AC136270/c
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                                                                                                                                                                                     /protein_id="BAC12811.1"
/db_xref="GI:22776536"
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SSNYMIRNYDYHPKTYEGRLVLFQPTDTGLTTIGPSQRITGRLDGMNQYGLVLGYNFT
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 312728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 11, 2003_this sequence version replaced gi:27368635.
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Homo sapiens chromosome l clone RP11-619A13.
BX005159
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Center: Wellcome Trust Sanger Institute
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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HTG; HTGS_PHASE2; HTGS_CANCELLED.
Homo sapiens (human)
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5593. .7476
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LOCUS
DEFINITION
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331221 bp DNA linear HTG 23-NOV-2002 ***, 12 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers

1 312728: contig of 312728 bp in length.

Location/Qualifiers

1 312728: Days in length.
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 167037 bases at least Q40
Consensus quality: 167127 bases at least Q30
Consensus quality: 167126 bases at least Q30
Insert size: 312728; sum-of-contigs
Insert size: 161110; 3.9% error; agarose-fp
Quality coverage: 4.11x in Q20 bases; sum-of-contigs Quality
coverage: 8.01x in Q20 bases; agarose-fp
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HTG; HTGS_PHASEL; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="assembly_fragment:01914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19078 TIGIGGALCTIGIGAGGAGTGATIGGCT 19051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="RPCI-11.3"
1. .312728
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Best Local Similarity 82.13
Matches 23; Conservative
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are unknown. This record will be updated with the finished sequence.
                                       Consensus quality: 257314 bases at least Q40 Consensus quality: 255389 bases at least Q30 Consensus quality: 271049 bases at least Q20 Estimated insert size: 267830; sum-of-contigs estimation Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
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320549: gap of unknown length
322012: contig of 1463 bp in length
122112: gap of unknown length
324044: contig of 1932 bp in length
324144: gap of unknown length
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328550: contig of 4406 bp in length
328650: gap of unknown length
331221: contig of 2571 bp in length.
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/note="wgs_contig"
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44136. .245292
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:62543. .263907
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152455. .154397
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158417. .160948
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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P. Ferser, C. Gabisi, A., Ganta, R., Garcia, A., Garca, M., Gebregeorgis, E., Gear, K., Gill, R., Grady, M., Guerra, W., Guevara, M., Guararie, P., Haadland, W., Hamil, C., Hamilton, C., Hamilton, K., Hariandez, R., Hines, S., Haddun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlabird, D., Jackson, A., Jackson, L., Jang, H., Ohnson, B., Johnson, R., Liu, Y., Lobow, H., Levan, J., Lewais, L., Liz, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Machen, E., Manden, E., Martinez, E., Manden, L., Mahindarte, M., Martine, R., Martinez, E., Manden, L., Marker, G., Martine, S., Mulandiasa, M., Martinez, E., Manden, D., Okuvonu, G., Olarnpunsagoon, M., Pal, S., Parks, K., Martine, S., Mulandiasa, M., Pal, S., Parks, K., Pareter, M., Redier, M., Redier, S., Paul, H., Perez, A., Perez, L., Perankoch, C., Rodkey, T., Robovic, D., Primus, E., Peul, L.-L., Pasternak, S., Paul, H., Perez, A., Perez, M., Redier, S., Riggs, F., Reilly, M., Ren, Y., Redier, M., Richards, S., Riggs, F., Sanders, M., Saverty, G., Scherer, S., Socott, G., Shatsman, S., Shen, H., Sherty, J., Sheath, M., Saverty, G., Scherer, S., Socott, G., Shatsman, S., Shen, H., Saverty, G., Scherer, S., Socott, G., Walse, R., Wang, C., Ward, R., Wang, C., Ward, R., Walse, R., Wal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 23, 2002 this sequence version replaced gi:24431541.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Center: Baylor College of Medicine
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Rat Genome Sequencing Consortium.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                          Hypocrea jecorina
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreacemycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 5359)
Seiboth, B., Hofmann, G. and Kubicek, C. P.
Lactose metabolism and cellulase production in Hypocrea jecorina:
the 9417 gene, encoding galactose-1-phosphate uridylyltransferase,
is essential for growth on galactose but not for cellulase
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Seiboth, B., Hofmann, G. and Kubicek, C.P.
Direct Submission
Submitsed (09-JAN-2002) IBTM, TU Vienna, Getreidemarkt 9, Vienna 1060, Austria
Sequence update by submitter
on Jan 9, 2002 this sequence version replaced gi:16209627.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-SEP-2001) IBTM, TU Vienna, Getreidemarkt 9, Vienna
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/gene="ada2"
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Seiboth, B., Hofmann, G. and Kubicek, C.P.
Direct Submission
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197084 CTAGGATTCTGTCAAGAGGGATAGGCTG 197057
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CYAAYHHLGPVYNIAIWTVVVALGHFASELFVFKSWTFGLFQIFPFFLATTALIWMP
LVRSHYVEFE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="transmembrane domain-containing protein" complement (join (4623. .5072,5146. .5208)) (gene="erg28" / hote="Erg28" similar to the Erg28p of Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join(<4623. .5072,5146. .>5208))
/gene="erg28"
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number="2.7.7.12"
                             /note="Gal7"
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AC020676 Homo sapi
AC103891 Homo sapi
AC103891 Homo sapi
AC103891 Homo sapi
AC125238 Homo sapi
AC125238 Homo sapi
AC122833 Homo sapi
AC122833 Mus muscu
AC13492 Rattus no
AC141426 Mus muscu
AC141426 Mus muscu
AC100967 Rattus no
AC100967 Rattus no
AC100967 Homo sapi
AC110917 Mus muscu
AC110917 Mus muscu
AC110917 Mus muscu
AC10172 Homo sapi
X78823 S.ccidenta
BX935170 Gallus ga
AL831875 Homo sapi
BX935170 Gallus ga
AL831875 Homo sapi
BD246112 Developme
BD246112 Developme
BD246112 Developme
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1P 2005524081-A/7
06-AUG-2002
03-SEP-1999 JP 2000568998
04-SEP-1999 US 60/099138
MICHEL SADELAIN,NEIL H BANDER,MICHAEL GONG
CLENIS/09,A6IK35/26,A6IK35/76,A6IK39/395,A6IK48/00,A6IP35/00,CO7K19/00,A6IK35/26,A6IK35/76,A6IK39/395,A6IK48/00,A6IP35/00,CI2NIS/00,CO7K19/00,CO7K16/44,CI2NIS/00,CI2NS/10)
CLENIS/10/CO7K16/44,CI2NIS/00,CI2NS/10
Fused receptor specific to prostate-specific membrane antigen and its use
                                                                                                                                                                                                                                                                                                                                                                      BD272284.1 GI:33082052
JP 2002524081-A/7.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 27)
Sadelain,M., Bander,N.H. and Gong,M.
                                                                                                                                                                                                                                                                                                                                          Rused receptor specific to prostate-specific membrane antigen and
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       its use
Patent: JP 2002524081-A)7 06-AUG-2002;
SLOAN KETTERING_INSTITUTE FOR CANCER RESEARCH
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    .27
    forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

                                                                                                                                                                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                 27 bp
                      AC103881
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AC110917
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AC109678
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AC010172
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BD246111
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AC129421
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AC102369 Mus muscu
AC12359 Mus muscu
AC12359 Mus muscu
AC125598 Sequence
AUS17504 Homo sapi
BD267803 Methods a
107254 Sequence 11
AR380771 Sequence
BD015187 TLi5a cel
J02988 Human T-cel
AX557214 Sequence
AX657214 Sequence
AX657214 Sequence
AX65881 Sequence
AX65881 Sequence
AX63559 Sequence
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                                                                                                                                                                                                    9053458
           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                4526729 seqs, 23644849745 residues
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Maximum Match 100%
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AR380771
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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gbb_htg:..
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Center: Whitehead Institute/MIT Center for Genome Research
                                            Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
    All repeats were identified using RepeatMasker:
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,
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McClean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,
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Wurphy, T., Naylor, J., Maylor, J., Maylor, J., Micol, R.,
Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R.,
Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Traverer, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,
Direct, Submission,
Direct Submission
                                                                                                                                                                                                                                                                           HTG 25-MAR-2004
*** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 189912)
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                                                                                                                                                                                                                                                                                                           Mus musculus chromosome 12 clone RP24-12016 map 12, IN PROGRESS ***, 5 unordered pieces.
                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                    ACI02434.4 GI:45736689
HTG; HTGS PHASE1; HTGS FULLTOP; HTGS ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 12, clone RP24-12016
GCGGCCGCAATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                   189912 bp
                                            1 GCGGCCGCAATTGAAGTTATGTATCCT
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 214580)
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                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 189912;
                                                                                                                                                                                                                                                                                                                                                                                                                                         60150: contig of 60150 bp in length
60250: gap of 100 bp
94286: contig of 34036 bp in length
94386: app of 100 bp
98686: contig of 4300 bp in length
98786: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 142004: contig of 43218 bp in length 5 142104; gap of 100 bp 5 189912: contig of 47808 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
-------- Project Information
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Mus musculus chromosome 12, clone RP23-246F14
Unpublished
2 (bases 1 to 214580)
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/clone="RP24-120L6"
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Pred. No. 2.6e+02;
0; Mismatches 3;
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106805 GGCCTCAATTGCAGATATGTATCC 106782
                                                                                                                  Center project name: L18789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNP
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/chromosome="12"
                                                                                                                                                  Center clone name: 120 L 6
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AC102369.21 GI:48059446
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Best Local Similarity 87.5%;
Matches 21; Conservative
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94287
94387
98687
98787
142005
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Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacGonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mihova, T., O'Connor, T., O'Donnell, P., O'Norbil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riebesk, M., Riley, R., Schauer, S., Schupback, R., Seman, J., Roserti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stams, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Stauss, N., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G., Suhiston, S., Subsision
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Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 214580)
Si Inten, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Choepel, Y., Collymore, A., Cocke, P., Collymore, J., Boukhgalter, B., Candara, J., Erickson, J., Erickson, J., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad-Toh, K., Liu, G., Liu, X., Luil, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Macdonald, P., Major, J., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Nicol, R., Schupback, R., Seevery, P., Roman, J., Schube, M., Taversa, M., Vaschilev, J., Peterson, K., Schube, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vascillev, H., Venkataraman, V.S., Viel, R., Voller, R., Lamer, A., and Zody, M. Direct Submission, M., Vannell, P., Voller, M., Venkataraman, V.S., Viel, R., Venkataraman, V.S., Viel, R., Venkataraman, V.S., Submission, M., Vannell, P., Venkataraman, V.S., Viel, R., Venkataraman, V.S., Submission, M., Vannell, M., Venkataraman, V.S., Submission, M., Venkataraman, V.S., Submission, M., Venkataraman, V.S., Submission, M., Venkataraman, V.S., Viel, R., Venkataraman, V.S., Viel, R., Venkataraman, V.S., Submission, M., Venkataraman, V.S., Viel, R., Venkat
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
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JOURNAL
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complement(1. .2178)
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2841, .2993
-/rpt_family="MBR73"
3052, .3086
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complement (3966, .4048) family="BlF" [8. 13055 . .15315) organism="Mus musculus" /rpt family="ID4" 4066. 4092 complement (4181. .4330) /rpt_family="B3A" 6284. .6339 /rpt_family="(CAAAAA)n" 16640. .16996 /rpt family="(TCTCTG)n" complement (7756. .8044) /rpt_family="B4" 8402. .8681 /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="12" /rpt_family="AT_rich"
7268. .7417
/rpt_family="L1MDa"
7580. .7600 /rpt_family="Lx6" 17007. .17055 /rpt_family="(CAAAA)n" 17090. .17606 family="(GGGTG)n" /rpt_family="(TTAA)n" 4093_ .4175 /rpt_family="(TTCC)n" /note="clone_boundary clone_end:SP6 site:EcoR1" rpt_family="AT_rich" for . 7691 rpt_family="(TCTG)n" (596. .7725 /rpt_family="(CAAA)n" complement(15199. 15 'rpt_family="MLT1G3" .6201. .16394 'rpt_family="B1_MM" 3901. .13961 Location/Qualifiers /rpt_family="MTD" family="Lx2" .13900 .214580 /map="12 rpt_far 3766. rpt<u>f</u>a 2768. repeat_region

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/organism="Mus musculus"
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Center clone name: 501_B_5
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Cook, N. Boariance

Cook, N. Choepel, Y. Colangelo, M. Collins, S. Collymore, N. Cook, P. Dearellano, K. Dewar, K. Diaz, J.S. Dodge, S. Farreira, P. Fitzgradd, M. FitzHugh, W. Gage, D. Galagan, J. Gardyna, S. Gande, S., Gord, S., Goyette, M. Graham, L., Grand-Pierre, N. Hagos, B., Horton, L., Hulme, W. Iliev, I. Lancoque, K. Lamazares, R., Landers, T., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Lind, G. Macdonald, P., Major, J., Marquis, N., Marthews, C., McCarthy, M. McEwan, P., Mackernan, K., Meldrim, J., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Morman, C.H., O'Connor, T., O'Donnell, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. L (bases 1 to 245862)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 12, clone RP24-501E5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.1%; Score 19.2; DB 10; Length 214580; 87.5%; Pred. No. 2.6e+02; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC123598
AC123598.4 GI:42761736
HTG; HTGS_PHASB1; HTGS_FULITOP; HTGS_ACTIVEFIN. Was musculus (house mouse)
                                                                                                                                                                                                                                                                                                       complement (2039).
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complement(21904. .22282)
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complement(22283. .22499)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt family="AT rich"
complement (21486. .21826)
rpt family="Lx8"
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8929. .19138
                                                                                                                                                                                                                                                                                           rpt_family="RLTR10C"
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                    rpt_family="L1_MM" 7950. .17993
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Conservative
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TITLE
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REFERENCE
AUTHORS
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O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Stohupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Travodore,J., Tophan,K., Travers,M., Travis,N., Trigilio,J., Vossilico,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission

Submitted (Ol-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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19404: gap of 100 bp

41155: gap of 100 bp

41255: gap of 100 bp

155335: contig of 114080 bp in length

155435: gap of 100 bp

155405: gap of 100 bp

165910: contig of 10475 bp in length

166010: gap of 100 bp

184580: contig of 18470 bp in length

212061: contig of 27481 bp in length

212161: gap of 100 bp

212161: gap of 100 bp

212161: contig of 27481 bp in length

212161: contig of 33701 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Gaps

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/PGPSREPANTNLVVGTDIYFCKIEVMYPPPRDFAATRS"
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Submitted (19-NOV-2002) Gan S.U., Molecular Medicine, GKT School of
Medicine and Dentistry, Rayne Institute, 123 Coldharbour Lane,
London SES 9NV, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              HSA517504 705 bp mRNA linear PRI 01-SEP-2003
Homo sapiens mRNA for T-cell-specific surface glycoprotein (CD28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gan, S.U., Hare, J., Krivoshchapov, L., Hui, K.M., Galea-Lauri, J.,
Farzaneh, F. and Darling, D.
New human CD28 isoforms generated by a novel splicing event in the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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alternative splicing; CD28 gene; T-cell-specific surface
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Morris,D.W. and Engelhard,E.K.
Novel compositions and methods for cancer
Patent: WO 03008583-A 1510 30-JAN-2003;
Sagres Discovery (US)
Location/Qualifiers
                                                                                                                            /organism="Homo sapiens"
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AJ517504
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2 (bases 1 to 705)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Lee K.P., Taylor, C., Petryniak, B., Turka, L.A., June, C.H. and Thompson, C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The genomic organization of the CD28 gene, Implications for the regulation of CD28 mRNA expression and heterogeneity J. Immunol. 145 (1), 344-352 (1990)
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Human דיכell membrane glycoprotein CD28 mRNA, exon 2.
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                                      /map="12"
/clone="RP24-501ES"
/clone_lib="RPC1-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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order(M37812.1:813. .984,1. .64)
/gene="CD28"
                                                                                                                               ch 71.1%; Score 19.2; DB 2; 1 Similarity 87.5%; Pred. No. 2.7e+02; 21; Conservative 0; Mismatches 3;
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 /db_xref="taxon:10090"
/chromosome="12"
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/note="G00-118-765"
/number=2
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100.0%; Pr
tive 0;
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glycoprotein CD28.
2 of 4
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JP 2001157592-A/5
12-JUN-2001
04-OCT-2000 JP 2000305557
13-JUL-1990 US
BRIAN SEED, ALEJANDRO ARUPFO, MARTIN AMIOT
C12N15/09, COTK14/725, G01N33/53, C12N15/00
TLiSa cell surface antigen and CD27 cell surface antigen, and utilization
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1 (bases 1 to 1514)
Seed, B., Aruffo, A. and Amiot, M.
TLiSa cell surface antigen and CD27 cell surface antigen, and trilization thereof.
Patent: JP 2001157592-A 5 12-JUN-2001,
                                                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 1514)

2 (cocks, B.G., Stuart, S.G. and Seilhamer, J.J.

Compositions for the detection of blood cell and immunological response gene expression

Patent: US 6607879-A 1316 19-AUG-2003;

Location/Qualifiers
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TLiSa cell surface antigen and CD27 cell surface antigen, and
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   70.4%; Score 19; DB 6; Length 1514; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
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Location/Qualifiers

    1514
    /organism="Homo sapiens"
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    1514
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                                                                                              438 AATTGAAGTTATGTATCCT 456
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                                                                         9 AATTGAAGTTATGTATCCT 27
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JP 2001157592-A/5.
Homo sapiens (human)
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                                      19; Conservative
                    Best Local Similarity
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                                                                                                                                                                                                                                                                             Methods and products related to metabolic interactions in disease
Datent: JP 2002512203-A 6 23-APR-2002;
THE UNIVERSITY OF VERMONT AND STATE AGRICULTURAL COLLEGE
OS Homo sapiens (human)
PD 23-APR-2002
PF 30-MAR-1999 US 60/082250,29-JUL-1998 US 60/094519 PR
24-SEP-1998 US 60/082250,29-JUL-1998 US 60/094519 PR
PC AGIK39/395,AGIK31/519,AGIK31/55,AGIK31/704,AGIK31/7056,AGIK31/PPC
PC AGIK39/17,AGIK38/21,AGIK45/06,AGIP3/10,AGIP35/00,CIZN15/00, PC
GOIN33/574,
                                                                             ырсел803 1514 bp DNA linear PAT 17-JUL-2003
Methods and products related to metabolic interactions in disease.
BD267803
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (basel to 1514)
Newell, M.K.
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Seed, B.D.Do. M. B., Allen, J., Aruffo, A., Camerini, D., Lauffer, L.D.,
Seed, B.D.Do. M. B., Allen, J., Stumenkovic, I. and Stengelin, S.D.
Rapid immunoselection cloning method
Patent: EP 0330191-AZ 11 30-AUG-1989;
Location/Qualifiers
1. 1514
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Methods and products related to metabolic interactions in
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100.0%; Pred. No. 2...
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
381 AATTGAAGTTATGTATCCT 399
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Matches 19; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                         O'Hara,R.M. and Nagelin,A.M.
Agents that specifically block cd28-mediated signaling and uses therefor
Patent: WO 20066059-A 1 29-AUG-2002;
Genetics Institute, LLC (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 0;
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Novel compositions and methods for cancer
Partent: WW 03008583-A 1509 30-JAN-2003;
Sagres Discovery (US)
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Sequence 1509 from Patent W003008583.
AX695882 GI:29419047
                                                    DNA
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
                                             3803 bp
Sequence 1 from Patent WO02066059.
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/organism="Homo sapiens"
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                                                                                                     AX557214.1 GI:25900195
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/codon start=1
/protein id="AAA60581.1"
/db xref="GDB:63045"
/db xref="GDB:6300-118-765"
/translation="MLRLLIALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSY
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YVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVG
GVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMMTPRRPGFTRKHYQPYAPPRDFAAY
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Human T-cell-specific homodimer surface protein CD28 mRNA, complete
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Draft entry and computer-readable sequence for [1] kindly provided by B.Seed, 11-AUG-1987.
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1514)

Aruffo,A. and Seed,B.

Molecular cloning of a CD28 cDNA by a high-efficiency COS cell expression system

Proc. Natl. Acad. Sci. U.S.A. 84 (23), 8573-8577 (1987)
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/note="T-cell-specific homodimer surface protein signal
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/gene="CD28"
/product="T-cell-specific homodimer surface protein"
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                                                Query Match 70.4%; Score 19; DB 6; Length 1514; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 19; Conservative 0; Mismatches 0; Indels
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T-call-specific homodimer surface protein.
Homo sapiens (human)
Homo sapiens
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                                                                                                                  438 AATTGAAGTTATGTATCCT 456
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 66887)

2 Ling, V., Wu, P. W., Finnerty, H.F., Agostino, M.J., Graham, J.R., Chen, S., Jussiff, J.M., Fisk, G.J., Miller, C.P. and Collins, M. Assembly and Annotation of Human Chromosome 2q33 Sequence Containing the CD28, CTLA4, and ICOS Gene Cluster: Analysis by Computational, Comparative, and Microarray Approaches

L Genomics 78 (3), 155-168 (2001)

11735222

2 (bases 1 to 66887)

Ling, V., Wu, P.W., Finnerty, H.F., Agostino, M.J., Graham, J.R., Chen, S., Jussiff, J., Fisk, G.J., Miller, C.P. and Collins, M. Direct Submission

L Submitted (15-AUG-2001) Department of Immunology, Genetics

Institute/Wyeth Research, 200 Cambridge Park Drive, Cambridge, MA
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/protein id="AAL40331.1"
/db_xref="G1:"7646226"
/translation="MLRLLIALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKXSY
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                           66887 bp DNA linear PRI 13-DEC-2004 down sapiens clone BAC_22606 CD28 antigen (CD28) gene, exons 1, 2 AF411057
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7838. .8329—
/note="sinilar to NADH:ubiquinone oxidoreductase"
42348. .>66887
/gene="CD28"
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gene="CD28"
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
Novel compositions and methods for cancer
Patent: WO 03008583-A 1508 30-JAN-2003;
Sagres Discovery (US)
Location/Qualifiers

    .51365
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
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gene="CD28"
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/organism="Homo sapiens"
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/gene="CD28"
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                                                                                                        Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bluestone, J.A., Collins, M., Whitters, M., Griffin, M. and Kranz, D. Surface-bound antigen binding portions of antibodies that bind to cata-4 and ca28 and uses therefor Patent: WO 0179300-A 3 25-OCT-2001; GENETICS INSTITUTE, INC. (US)

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 02068579-A 1803 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 1508 from Patent W003008583.
AX695881
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                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3 from Patent W00179300,
AX283559
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      Homo sapiens (human)
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Best Local Similarity
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Elizabea 1 to 88624)

Sincero, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Porlins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gadse, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Mandonal, T., Landerer, T., Lehorczky, J., Levine, R., Lieut, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivart, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:6682672.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens clone RP11-8P23, LOW-PASS SEQUENCE SAMPLING.
ACO20676
HTG; HTG:9123792
NLFSREFRASLHKGLDSAVEVCVYGNYSQQLQVYSKTGFNCDGKLGNESVTFYLQNL
YVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVG
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Contact: sequence submissions@genome.wi.mit.edu
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                                                  GVLACYSLLVTVAFIIFW"
62505. .62861
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved. 982: contig of 882 bp in length 1986: contig of 904 bp in length 1986: contig of 904 bp in length 1986: contig of 904 bp in length 3005: gap of 100 bp 2905: contig of 919 bp in length 4003: gap of 100 bp 5022; contig of 922 bp in length 6024: gap of 100 bp p in length 6020: contig of 912 bp in length 6020: contig of 914 bp in length 6020: contig of 914 bp in length 6020: contig of 914 bp in length 6020: gap of 100 bp p in length 6020: contig of 914 bp in length 6020: contig of 910 bp in length 6020: contig of 910 bp in length 6020: contig of 910 bp in length 6020: contig of 902 bp in length 6020: contig of 902 bp in length 6020: gap of 100 bp p in length 6020: contig of 909 bp in length 6020: contig of 909 bp in length 6000: contig of 900 bp in length 6000: con 1: gap of 100 bp 1: contig of 910 bp in length 1: gap of 100 bp 1: contig of 897 bp in length 1: gap of 100 bp o: gap of 100 bp 1: contig of 893 bp in length 1: gap of 100 bp 1: contig of 918 bp in length 2: gap of 100 bp in length , o bp of 915 bp iv 100 bp contig gap of 10908: 11008: 11921: 14949: 15049: 26100: 27013: 33064: 33164: 13947: 12021: 12931: 13031: 14047: 5960: .0909 6971: 7996: 18096: 8986: 19086: 20958: 21948: 22048: 23057: 23967: 24067: 25001: 25101: 26000: 27113: 28031: 29041: 29141: 30038: 31031; 32049: 32149: 18987 19983 20093 20093 21059 21059 21049 22049 22958 23958 24068 25002 25102 28132 29142 30039 30139 31032 26001 26101 27014 28032 31132 32050 32150 33065

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entries of 925 bp in length agap of 100 bp in length is gap of 100 bp in length is contig of 916 bp in length contig of 929 bp in length agap of 100 bp in length is contig of 896 bp in length agap of 100 bp in length is gap of 100 bp in length agap of 100 bp in length is gap of 100 bp.
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contig of 906 bp in length
gap of 100 bp pin length
gap of 100 bp in length
contig of 912 bp in length
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, B., Beda, F., Bada, F., Baldwin, J., Barna, N., Beda, F., Beda, F., Bodubgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dakrellano, K., Domino, M., Doyle, M., Doyle, M., Caladan, G., Gant, G., Hagos, B., Heaford, A., Horton, L., Rensetor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Lovine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Morman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pistani, C., Polnara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Liench, Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome Submitted (08-JAN-2000) Whitehead Institute/MIT Center for Genome Submitted (08-JAN-2000) Whitehead Lusing RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp:genome.washington.edu/RM/RepeatMasker:html
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HOMO SADIENS CLONE RP11-8P23, LOW-PASS SEQUENCE SAMPLING.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
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                                                                                                        70.4%; Score 19; DB 2; Length 88624; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels (
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L2295
70504: gap of 100 bp
71416: contig of 912 bp in length
71516: gap of 100 bp
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
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                                                                                                                                                                                                                                  9 AATTGAAGTTATGTATCCT 27
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HTG; HTGS PHASE0.
Homo sapiens (human)
                                                                                                           Query Match
Best Local Similarity 100."
Matches 19; Conservative
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           70405
70505
71417
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of 904 bp in] of 904 bp in]	100 bp _ of 919 bp in	100 bp to in 50 in	100 bp _ of 922 bp	100 bp of 899 bp	100 bp of 913 bp	of 912 bp	of 871 bp	of 874 bp	of 914 bp	of 913 bp	of 910 bp	100 pp of 916 bp	of 902 bp	of 911 bp	100 pp of 911 bp	100 bp of 925 bp	100 pp of 890 pp	100 bp of 906 bp	of 866 bp	of 890 bp	of 909 bp	of 910 bp	of 934 bp	dq 668 jo	100 pp of 913 bp	100 bp of 918 bp	100 bp of 910 bp	100 bp of 897 bp	100 bp of 893 bp	100 bp	or 918 pp 100 bp	of 915 bp	of 906 bp	100 bp of 924 bp	100 bp of 932 bp 100 bp
i ii	gap of 100 bp contig of 919 bp in	gap of 100 bp contiq of 898 bp in	gap of 100 bp contig of 922 bp	gap of 100 bp contig of 899 bp	gap of 100 bp contig of 913 bp	contig of 912 bp	contig of 871 bp	contig of 874 bp	gap of 100 bp contig of 914 bp	contig of 913 bp	contig of 910 bp	gap or 100 pp contig of 916 bp	contig of 902 bp	contig of 911 bp	gap of 100 bp contig of 911 bp	gap of 100 bp contig of 925 bp	gap of 100 bp contig of 890 bp	gap of 100 bp contig of 906 bp	contig of 866 bp	contig of 890 bp	contig of 909 bp	contig of 910 bp	contig of 934 bp	gap of 100 pp contig of 899 bp	gap of 100 bp contig of 913 bp	gap of 100 bp contig of 918 bp	gap of 100 bp contig of 910 bp	gap of 100 bp contig of 897 bp	gap of 100 bp	gap of 100 bp	gap of 100 bp	contig of 915 bp	contig of 906 bp	gap of 100 bp contig of 924 bp	gap of 100 bp contig of 932 bp gap of 100 bp
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81561. .01913 human STS CHLC.GGAA 19E07.P17317 clone
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7055 ... 30783

700te="L18270 Human chromosome 2 STS UT426"
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(Dases I to 106539)

Fitzpatrick, E.S., Hammond, H.A., DeAngelis, D.M., Soderman, A.R., Wright, J.L., Liu, X., Larson, D., McGowan, J., Ziegler, S., Pritchard, L., Hess, J.F., Todd, J., Caskey, C.T. and Metzker, M.L. Bliect Submitssion
Submitted (18-JAN-2000) Department of Human Genetics, Merck & Co., Inc., SunneyTown Pike, West Point, PA 19486, USA
                                                                                                                         AF225899 106539 bp DNA linear
Homo sapiens PAC clone 219d7, complete sequence.
AF225899
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
AUTHORS
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 108100)
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Homo sapiens BAC clone RP11-638D14 from 2, complete sequence.
AC103881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              family="THE1"
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82595. .82857
/rpt_family="Alu"
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complement(86698.
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1058<u>9</u>1. .106161
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Homo sapiens
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Matches 19; Conservative
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AC103881
LOCUS
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KEYWORDS
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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Submitted (23-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 23, 2002 this sequence version replaced giil8030160.
                                                                                                                                                                                                                                                                   Submitted (29-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 61108, USA
4 (bases 1 to 108100)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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The clone sequenced to the left is RP11-789A18, 2000 bp overlap,
the clone sequenced to the right is RP11-515K12, 2000 bp overlap.
Actual start of this clone is at base position 146042 of
RP11-789A18; actual end is at base position 23686 of RP11-515K12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A transposon was identified in a growth of the clone RP11-638D14, which is not a part of the submitted sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphisms have been identified between AC093113 and AC103881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center
                        Levy, A., Kozlowicz, A. and Spalding, L.
The sequence of Homo sapiens BAC clone RP11-638D14
Unpublished (2001)
3 (bases 1 to 108100)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WUGSC
2 (bases 1 to 108100)
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rpt family="L1"
12300. 12779
rpt family="L1"
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CK407559 148587 bp DNA linear HTG 11-AUG-2004
Danio rerio clone CH211-283G2, WORKING DRAFT SEQUENCE.
CR407559
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Direct Submission
Direct Submission
Submitted (10-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 4, 2004 this sequence version replaced gi:50724958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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HTG; HTGS PHASE2; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Danio verio (zebrafish)
Danio xerio
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CR407559
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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COMMENT

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[mperial Cancer Research Fund (ICRF), creator: Dean
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/note="LINE2"
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Submitted (27-SEP-1999) MPIMG, Abt.Lehrach, Max Planck Institut
Submitted (27-SEP-1999) MPIMG, Abt.Lehrach, Max Planck Institut
Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
Contig 01

1. 175518

1. 175519

Clone ICRFc104 3C29 received from the Resource Centre of the Human
Genome Project at the Max-Planck Institut for Molecular Genetics.
Clones ICRFc104 1352, ICRFc104 203D3, ICRFc104 47E10, and ICRFc104
49A7 received from A. Monaco.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Reinhardt, R. and Lehrach, H.
Unpublished
                                                                                                                                                    Assembly program: XGAP4; version 4.5 Chemistry: bye-terminator; 100% of reads Consensus quality: 14858 bases at least Q40 Consensus quality: 148587 bases at least Q20 Consensus quality: 148587 bases at least Q20 Insert size: 148587; sum-of-contigs Insert size: 163547; 10.1% error; agarose-fp Quality coverage: 11.56x in Q20 bases; sum-of-contigs Quality coverage: 11.33x in Q20 bases; agarose-fp
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* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Submitted (16-AUG-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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AC125238
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sulston, 0. E. and Waterston, N. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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                                                            Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Porrest Park Avenue, St. Louis, Missouri 63108, USA and 16, 2002 this sequence version replaced gi:22138709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A transposon was identified in the finished region of this clone and removed prior to submission. The transposon would insert after base pair 83916 of this sequence.
                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                            clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence from base 156374 to base 156453 was derived from one plasmid subclone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of the clone. This clone is overlapped by AC069314 and AC010138.
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Location/Qualifiers
                                                                                                                                            Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                  Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0711C24
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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215. .236
/rpt_family="(TTTTA)n"
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    6 (bases 1 to 196622)
Waterston, R.
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                                                Direct Submission
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Standard, D. Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alebrooks, S., Amin, A., Anguiano, D., Allen, H., Alebrooks, S., Amin, A., Anguiano, D., Allen, H., Abyadi, A., Ayodei, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Caleron, B., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chavez, D., Chen, G., Chen, T., Chen, Z., Chacko, J., Chavez, D., Chen, G., Chen, R., Cree, A., D'Souza, L., Davis, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dermon, C., Dinh, H., Divya, K., Draper, H., Duya, F., Durn, A., Durbin, K., Duval, B., Eaves, K., Esotto, M., Esotto, M., Ewotto, M., Furbandez, S., Chingy, M., Flaggi, N., Forbesi, J., Foster, M., Garza, M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gunareno, P., Haaland, W., Hanli, C., Hamilton, C., Hamilton, K., Harnandez, S., Hadu, S.L., Hodgson, A., Hernandez, M., Hanes, S., Hladu, S.L., Hodgson, M., Hanies, S., Hladu, S.L., Hodgson, M., Johnson, R., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Manjan, M., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, Y., Luiw, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, Y., Luiw, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, Y., London, P., Mangum, B., Manjan, P., Martin, R., Martin, R., Martin, R., Manjum, P., Morris, K., Morris, S., Munten, M., Morris, S., Murtin, S., Murtin, S., Mullosavijevic, A., Minner, G., Minnia, B., Morris, S., Mullosavijevic, A., Minner, G., Minnia, M., Murphy, M., Nauly, M., Nauly, M., Nauly, M., Nauly, M., Martin, S., Mullosavijevic, A., Minner, G., Minnia, M., Murphy, M., Martin, S., Mullosavijevic, A., Minner, S., 
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Rattus norvegicus clone CH230-4C5, WORKING DRAFT SEQUENCE, 2
unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
/rpt_family="Alu"
12555. 12682
/rpt_family="MBR2_type"
12683. 13170
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13171. 13193
/rpt_family="MBR2_type"
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13621 .14034
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14683 .14966
/rpt family="L1"
14967 .15260
/rpt family="Alu"
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15251. 15303
/rot_family="L1"
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/rpt family="Alu"
16075. .16315
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KEYWORDS
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24818376.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the setimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Pooro, C.D., Primus, B., Pull.-L., Puszo, M., Quiroz, J., Rachlin, E., Reeves, K., Pagier, M. A., Reigh, R., Ruiz, C., Radkey, T., Rojas, A., Rose, M., Rose, M., Raiggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Savery, G., Scherer, S., Sorelle, R., Sorelle, R., Sorelle, R., Sorelle, R., Strong, R., Suton, A., Savete, A., Trejos, Z., Usmani, K., Valas, R., Veray, V., Villasana, D., Walter, R., Walker, B., Wang, J., Wallson, R., Walte, R., Wallson, R., Smith, D., Von Niederhausern, A., Weiss, R., Smith, D., Yu, Smith, H.O., Weinstock, G. and Gibbs, R.A., Smith, D.R., Holt, R.A., Smith, D., Willson, R., Long, S., Long, S.,
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* See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* CONE: This is a "working draft' sequence it currently

* CONE: This is a "working draft' sequence is a consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Subract Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Huouston, TX 77030, USA
Baylor Plaza, Huot 235811)
Rat Genome Sequencing Consortium.
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Center code: BCW
Center code: BCW
Center code: Lttp://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: Project Information
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Submitted (05-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jun 21, 2002 this sequence version replaced gi:21206493.
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MCPherson, J. D. and Waterston, R.H.
Submission
Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park
                                                                  discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, Washu). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml VECTOR: pTARBAC2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 200339)
Levy,A. and Haglund,K.
The sequence of Mus musculus BAC clone RP23-181J12
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkway, St. Louis, MO 63108, USA (bases 1 to 200339)
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                                                  Repeat names beginning 'Dr' were identified by the Recon repeat
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Mus musculus BAC clone RP23-181J12 from 15, complete sequence.
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this is found the longest good quality representation will be
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Pred. No. 5.2e+02;
0; Mismatches 4;
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Contact: submissions@watson.wustl.edu
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                                                                                                                                                                                                                                                1. .151552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing of Mus musculus
Unpublished (2001)
3 (Dases I to 200339)
McPharson, J. D. and Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.9%;
Best Local Similarity 84.0%;
Matches 21; Conservative (
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL954182 151552 bp DNA linear VRT 25-NOV-2003 Zebrafish DNA sequence from clone CH211-205N18 in linkage group 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 25, 2003 this sequence version replaced gi:38230013.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 235811;
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Pred. No. 3.4e+02;
0; Mismatches 5; Indels
5 235811: contig of 1037 bp in length.
Location/Qualifiers
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Center: Wellcome Trust Sanger Institute
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| Da xref="taxon:10116"
|/clone="CH230-4C5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12494 GTGCCTACAATTGAAGTTATTTATCCT 12520
                                                                                                                                                                           1. .1994
/note="wgs_end_extension
clone_end:T7"
complement (4914. .5613)
/note="clone_boundary
clone_end:T7
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Contact: zfish-help@sanger.ac.uk
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end_seguence: BH304146"
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Best Local Similarity 81.5%;
Matches 22; Conservative
                                                  1. .235811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequence.
AL954182
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AL954182/c
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clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu MAPPING INFORMATION: restriction digest.

SOURCE INFORMATION:
The RECI-23 BAC Library has been constructed by Kazutoyo Osegawa
and Minako Tateno in the laboratory of Pieter de Jong
(http://www.chori.org) from female C57BL/6J mouse kidney and/or
brain genomic DNA. The clone and detailed information can be
obtained from Research Genetics, Inc. (http://www.resgen.com) or
Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
1. .200339 /organism="Mus musculus" /mol type="genomic DNA" /db_xref="taxon:10090" /chromosome="15" 10122. .10208 /rpt_family="Malk" /rpt_family="Malk" 10291. .10748 /rpt_family="RMER15" 10911. .10979 /clone="RP23-181J12" /clone_lib="RPCI-23" 1. .1573 10911. .10979 /rpt_family="MaLR" 11369. .11600 /rpt_family="L1"
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repeat_region

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/note="wgs_contig"
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Allen, C., Allen, H. Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebech, W., Aoyagi, A., Ayodej, M., Baca, E., Baden, H.,
Baldan, D., Bandaranaike, D., Barber, M., Baranteed, M., Benahmed, F.,
Baldwin, D., Bandaranaike, D., Barber, M., Baranteed, M., Benahmed, F.,
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Bryant, M., Buhay, C., Cavazos, I., Ceasar, H., Center, A.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Bangan, A., Escotto, M., Eugene, C., Fvare, C., Fvare, M., Gerer, M., Elagy, M., Flagy, N., Porbes, L., Fonger, P.,
Fernandez, S., Finley, M., Flagy, N., Forbes, L., Fonger, T.,
Gunazatne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Hernandez, S., Hines, S., Hune, J., Indepird, D., Jackson, A.,
Jockson, L., Jacob, L., Jang, H., Johnson, B., Johnson, R., Johnson, R.,
Jorensubewa, L., Loulseegd, H., Lozado, R.J., Lui, X., Mangum, A.,
Mangum, B., Mapha, P., Martin, K., Martin, R., Martinez, E.,
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Pasternak, S., Paul, H., Perez, A., Perez, M., Reish, R., Sanders, W., Savery, G., Saberer, S., Soctt, G., Saketty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Sanders, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218328 bp DNA linear HTG 09-OCT-2002 Sattus norvegicus clone CH230-245A4, *** SEQUENCING IN PROGRESS AC121459
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HTG; HTGS_PHASEL; HTGS_BRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                Score 18.6; DB 10;
Pred. No. 5.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                               3 GGCCGCAATTGAAGTTATGTATCCT 27
40619. .40819
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4138. .41549
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41861. .42144
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42610. .43314
                                                                                                                                                                42610. .43314
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43354. .43450
/rpt_family="Alu"
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Best Local Similarity 84.09
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Worley, K.C.

Direct Submission

Molecular and Human Genetics, Baylor College of Medicine, One Submitted (18-MAY-2002) Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Sat Genome Sequencing Consortium.

Direct Submission

M. Direct Submission

No Plaza, Houston, TX 77030, USA

On Sep 14, 2002 this sequence version replaced gi:22450321.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgst.bcm.tmc.edu/projects/fart/). As a reault, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.

Contigs will be indicated in the feature table.
Steimle, M., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villsean, D., Waldron, L., Walker, B., Wang, J.,
Wallsan, G., Wallson, R., Wacren, R., Wei, X., White, F.,
Willson, R., Warzen, R., Wei, X., White, F.,
Wilhen, D., Wilson, R., Weiss, Y., Wooden, H., Worlay, K.,
Wight, D., Wright, R., Wu, J., Yakub, S., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhauserin, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
L Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently a consists of 2 contigs. The true order of the pieces in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 217012: contig of 217012 bp in length 217013 217112: gap of unknown length 217113 218328: contig of 1216 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
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Query Match

SOURCE ORGANISM

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

REFERENCE

AUTHORS TITLE JOURNAL

REFERENCE

TITLE JOURNAL

COMMENT

REFERENCE

REFERENCE AUTHORS TITLE

DEFINITION

AC141426

ACCESSION VERSION KEYWORDS

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SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Geneics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is overlapped by ACI10175 and ACI24414.
Location/Qualifiers
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36371. 36608
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36773. 36863
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http://genome.wustl.edu
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                                                                                                                                                                                                                                                                                                 AC141426 227835 bp DNA linear ROD 15-MAY-2004
Mus musculus BAC clone RP23-280114 from chromosome 12, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (14-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (14-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (14-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-MAY-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (12-MAY-2004) St. Louis, MO 63108, USA (12-MAY-2004) St. Milson, R.K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, formid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-MAY-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA OM May 12, 2004 this Sequence version replaced gi:28973968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nue musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 227835)

Trani,L., Bielicki,L. and Haakenson,W.

The sequence of Mus musculus BAC clone RP23-280114

Unpublished (2001)

2 (bases 1 to 227835)

McPherson,J.D. and Waterston,R.H.

Direct Submission
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
                                          Score 18.6; DB 2; Length 218328; Pred. No. 5.4e+02;
                                                                                            ö
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: M_BA0280114
                                                                                            0; Mismatches
                                                                                                                                                                      9436 GGCTACAATTGAAGTTTTGTGCT 9412
                                                                                                                                         3 GGCCGCAATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                        AC141426
AC141426.3 GI:47131342
                                             ch 68.9%;
1 Similarity 84.0%;
21; Conservative 0
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                                                                  Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vilson, R.K.
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Status.

18 Marzy, D. Marzie, Merzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Anin, A., Angulano, D., Allen, T., Alsbrooks, S., Anin, A., Barrie, M., Benahmed, F., Balark, D., Bandstanaike, D., Barder, S., Blark, D., Bardstan, S., Blark, D., Barrie, T., Ceasar, H., Center, A., Cardens, V., Carter, K., Cavazos, T., Ceasar, H., Center, A., Chacko, D., Chang, D., Chang, C., Burth, P., Burrell, K., Duyan, C., Covkell, R., Cox. Covle, M., Cree, A., D'Souzal, Devilla, M.L., Davis, C., Bury, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Deneng, S., Dunn, H., Duyan, C., Covkell, R., Cox. Covle, M., Cree, A., Polgar, R., Edgan, A., Garner, T., Garra, M., Gusvara, W., Gunzara, M., Gusvara, W., Gunzara, E., Geer, K., Gill, R., Card, M., Gusvara, W., Gunzara, E., Farser, C., Geler, R., Gilla, M., Carter, M., Gusvara, W., Gunzara, M., Gusvara, W., Gunzara, M., Gusvara, W., Gunzara, E., Havalk, P., Haves, A., Hanilton, C., Hamilton, K., Havilk, P., Haves, A., Hanilton, C., Hamilton, K., Havilk, P., Haves, A., Hanilton, C., Hamilton, K., Martin, M., Martin, K., Worts, C., Martin, R., Martin, K., Martin, R., Martin, K., Martin, R., Martin, K., Martin, S., Mardor, M., Martin, M., Martin, M., Martin, M., Martin, K., Martin, K., Martin, K., Martin, S., Martin, S., Martin, S., Martin, S., Martin, S., Martin, K., Martin, S., Martin, S., Martin, S., Martin, S., Martin, R., Martin, K., Martin, M., Mar
                                                                                                                   94 227929 bp DNA linear HTG 09-MAY-2003 norvegicus clone CH230-4N15, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                AC094794.4 GI:30466624
HTG: HTGS PHASE2; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
40133 GGCAGCTATTGAAGTTATCAATCCT 40157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 227929)
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                                                                                 RESULT 31
AC094794/c
                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                          DEFINITION
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                       'rpt_family="MaLR"
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                                                                               rpt family="L1"
11720. .42055
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13610. .43702
                                       family="ID"
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Gaps

Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One

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Namany, Daness I to 236612, I.

Rallen, C., Malen, H., Alsbrooks, S., Amin, A., Anguano, D., Anyalebechi, V., Aoyaqi, A., Angodeji, M., Baca, B., Baden, H., Balandranaike, D., Barber, M., Barneteadh, Benahmed, F., Bidden, V., Bandarnaike, D., Barber, M., Barneteadh, Benahmed, F., Bidden, V., Banden, B., Banden, B., Banden, B., Banden, M., Baca, B., Baden, H., Basado, K., Blark, Blarit, J., Blankenburg, K., Blyth, P., Brown, M., Bayat, M., Cener, A., Decker, J., Cardeno, V., Carer, K., Carder, M., Cener, A., Decker, J., Cardeno, J., Cardeno, V., Carter, K., Carder, M., Cener, J., Deramo, C., Coyle, Chen, Y., Chen, Y., Chen, Y., Carder, M., Carder, M., Carden, M., Cabisi, A., Carne, M., Garra, M., Harnandez, S., Filly, M., Flaggy, N., Forbes, L., Poster, M., Garra, M., Harnandez, S., Haldun, S.L., Henderson, N., Hernandez, M., Havalle, S., Halfdun, S.L., Hue, J., Liu, J., Liu, J., Liu, M., Liu, Y., London, P., London, B., Johnson, R., Mangum, M., Mahida, M., Malloy, M., Mally, M., Mal
                                                         AC109678 236612 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-89E12, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                   HTG; HTGS PHASEL; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                     ***, 8 unordered pieces.
AC109678
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                                                                                    Submitted (199 MAX-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:22771587.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 227929: contig of 227929 bp in length.
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Center code: BCM

    .227929
    /organism="Rattus norvegicus"

Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 227929)
Rat Genome Sequencing Consortium.
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/db_xref="taxon:10116"
/clone="CH230-4N15"
1. .3298
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Direct Submission

Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza. Houston, TX 77030, USA
ON NOV 9, 2002 this sequence version replaced gi:23321591.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990329
Consensus quality: 194770 bases at least Q40
Consensus quality: 194876 bases at least Q30
Consensus quality: 201735 bases at least Q30
Estimated insert size: 198707; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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/db_xref="taxon:10116"
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115868. .117101
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1236. .3571
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Misches | 17005="Wagg Contig Relative | 17005="Wagg Contig Misches |
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us-09-786-502a-7.rge

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(bases 1 to 290066)
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                                                                                                     Rattus norvegicus
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Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J. Topham, K., Travers, M., Vassiliev, H., Verkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (11-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 11, 2004 this sequence version replaced gi:51036443.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLZY#21 290066 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-62C13, *** SEQUENCING IN PROGRESS
***, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                            ------ Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 68.9%; Score 18.6; DB 2; Length 247100; 1 Similarity 84.0%; Pred. No. 5.4e+02; 21; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16605: contig of 16605 bp in length 16705: gap of unknown length 36450: contig of 19645 bp in length 36450: gap of unknown length 60038: contig of 23588 bp in length 60138: gap of unknown length 6529: contig of 5791 bp in length 66229: gap of unknown length 185201: gap of unknown length 127430: contig of 29072 bp in length 127430: contig of 32229 bp in length 13773: gap of unknown length 13773: contig of 5947 bp in length 133577: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 168546: gap of unknown length
7 247100: contig of 78554 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168446: contig of 34869 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="RP23-74L20"
clone_lib="RPCI-23 Female Mouse BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .247100
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L14656
Center clone name: 74_L_20
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Best Local Similarity
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60039
60139
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36351.
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AC129421/c
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HTG; HTGS PHARE; HTGS DARAT; HTGS ENRICHED.

ANGER Ratten norvegicus (Norway rat)

Norway (Norwais, Mathern M. Lee, Abramzon, S., Adams, C., Alder, J., Allen, H., Alabrooke, S., Mahm, A., Maylanno, D., Allen, H., Alabrooke, S., Mahm, A., Maylanno, D., Andersanika (Norwais, Mathern M. C., Balar, D., Barber, M. Barnsada, M. Banhmad, F., Bladaria, D., Balar, D., Cockrell, B., Cockrell, M. Barnsad, M., Banhmad, F., Balard, D., Danson, S., Hanes S., Hanes S., Hanes S., Hanes, J., Hanes, J., Hanes, J., Hadan, S., Hanes, J., Hanes, J.
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RESULT 35
AC009464/c
                                                                                                                                                                                                                                                                                                                                                                              The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas ssembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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40709: gap of unknown length
281950: contig of 241241 bp in length
283370: contig of 1320 bp in length
283370: contig of 1320 bp in length
283470: gap of unknown length
286776: contig of 2606 bp in length
286176: gap of unknown length
290066: contig of 3890 bp in length.
                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine Center code: BCM
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/db_xref="taxon:10116"
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32547. .33462
/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end_sequence:BH287162"
40710. .42036
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280810. .281950
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283471
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BURATYOLS, MELEZOS, Chordats, Craniats, Vertebrats, Euteleostomi, Mammalis, Eutheria, Primates; Catarrhini, Hominidae; Homo.

Mammalis, Eutheria, Primates; Catarrhini, Hominidae; Homo.

1. (Dasses 1 to 16696)

Marty, D.M., Adams, C., Adlo-Oduola, B., Ail.-Oman, F.R., Allen, C., Alabrocoks, S.L., Amartunge, H.C., Are, J.R., Ayele, M., Bande, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bunde, J., Burket, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J. Chavez, D., Cartor, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Cox, C., Coyle, M.D., Chowchry, I., Christopoulos, C. Coyle, M.D., Dathorne, S.R., David, R., Martis, R., Gao, J., Garria, A., Garner, T., Garza, N., Gill, R., Gao, J., Garria, A., Garner, T., Garza, N., Gill, R., Gao, J., Garria, A., Garner, T., Garza, N., Gill, R., Gao, J., Garria, R., Hande, S., Huba, S., Hande, S., Huba, S., Hande, S., Huba, S., Hande, S., Huba, S., Hander, S., Hande, S., Huba, S., Hande, S., Huba, S., Hande, S., Huba, S., Martin, R., Martin
AC009464 146945 bp DNA linear PRI 31-JAN-2003
Homo sapiens 12 BAC RP11-19E18 (Roswell Park Cancer Institute Human
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Submitted (01-DEC-1999) Human Genome Sequencing Center, Department
Submitted (10-DEC-1999) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 146945)
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                                                                      BAC Library) complete sequence.
                                                                                                                                      AC009464.8 GI:28173064
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Homo sapiens
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Gaps 0;

68.9%; Score 18.6; DB 2; Length 290066; ilarity 84.0%; Pred. No. 5.5e+02; Conservative 0; Mismatches 4; Indels 0;

Query Match Best Local Similarity Matches 21; Conserv 50228 GCGGCAGCAATTCTGGTTATGTATC 50204

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1 GCGGCCGCAATTGAAGTTATGTATC 25

TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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ACI10187
Mus musculus chromosome 7 clone RP24-541E23 map 7, WORKING DRAFT
ACI10187
ACI10187.5 GI:45430174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Limb8"
complement (9849. 10139)
/rpt_family="AluSx"
complement (10140. 10277)
/rpt_family="Limb8"
complement (10304. 10680)
/rpt_family="Limb3"
10681. 10927
/rpt_family="AluJ"
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complement(110990. .11244)
cpt_family="LIMB3"
complement(11249. .11871)
/rpt_family="LI"
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complement(12081. .12419)

/rpt_family="THBIB"

complement(12687. .12937)

/rpt_family="L1"

12941. .13226
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complement(13275. .13393)
/rpt_family="L2"
complement(13526. .13990)
/rpt_family="L2"
14980. i15014
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ement(1200)
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/rpt family="(TA)n"
complement(9164 ... 9450)
/rpt family="Aluy"
complement(9476 ... 9781)
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9785. .9805
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complement(9813..9848)
/rpt_family="LIMB8"
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15365. 15385
/rpt_family="AT_rich"
5231. .585?
                                                                                              5963. .6237
/rpt_family="AluSg"
6797. .7094
/rpt_family="AluJo"
/304. .7614
                                                                                                                                                                                                                                                                                                                                                                /rpr. cose6
/rpr. family="HAL1"
84137 .8724
/rpt. family="AluSx"
88687 .8941
                                                                           /rpt_family="L1ME3A"
5963. .6237
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9016. .9163
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8132. .8366
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Best Local Similarity 95.03
Matches 19; Conservative
      repeat_region
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DEFINITION
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VERSION
                                                                                                                 Direct Submission

Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

( bases 1 to 146945)

Morley, K.C.

Morley, K.C.

Morley, K.C.

Morley, K.C.

Morley, R.C.

Morley, M.C.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 146945) Worley, K.C.
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3511. .3648
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/standard_name="WI-16568"
851. .966
/standard_name="A010A40"
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/mol_type="genomic DNA"
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/chromosome="12"
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/rpt_family="T-rich"
3507, .362
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/rpt_family="(A)n"
3475. .3512
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STS

FEATURES

us-09-786-502a-7.rge

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as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented arbitrary but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                Consensus quality: 174704 bases at least Q40 consensus quality: 177216 bases at least Q30 Consensus quality: 178020 bases at least Q20 Insert size: 178000; agarose-fp consersize: 178494; sum-of-contigs Quality coverage: 8.0 in Q20 bases; sum-of-contigs Quality coverage: 8.0 in Q20 bases; sum-of-contigs
Chemistry: Dye-terminator Big Dye; 100% of reads
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: contig of 1500. ...
); gap of 100 bp
4; contig of 9205 bp in length
14; gap of 100 bp
14: gap of 3668 bp in length
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gap of 100 bp
contig of 2224 bp in length
gap of 100 bp
contig of 1693 bp in length
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gap of 100 bp
contig of 22527 bp in length
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contig of 23630 bp in length
gap of 100 bp
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gap of 100 bp
contig of 9342 bp in length.
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contig of 8739 bp in length
gap of 100 bp
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100 bp
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of 9207 bp in length
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30145. .38883
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62714. .64667
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1. .180254
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Diase, J., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Chang, J., Choppia, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J.,
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                    Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 7, clone RP24-541E23
     HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, J., Cook, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreitz, P., FitzGerad, M., Gage, D., Galdgan, J., Gardyna, S., Grander, L., Gardyna, S., Grander, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mahova, T., Mlenga, V., Murphy, T., Naylor, J., Nouyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Nell, D., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Schauer, S., Schupback, R., Seaman, S., Schupback, R., Seaman, S., Schupback, S., Schupback, R., Seaman, S., Stupback, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilliev, H., Vorbataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct, Subnission, M. Marin, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-PEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 193005)
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 122445
Center clone name: 155_1_20
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musiaes 1 to 193005)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-155120
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2 (bases I to 199432)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boqualavky, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Garand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, M., Illev, I., Johnson, R.,

Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,

Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,

Maclean, C., Macdonald, P., Major, J., Marphy, T., Naylor, J., Naylor, J.,

Macathy, M., McEwan, P., McKernan, K., MacPheeters, R., Meldrim, J.,

Mancus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Noryen, C.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Santos, R., Schupback, R.,

Seman, S., Severy, P., Spencer, B., Stanger, Theodore, J.,

Topham, K., Travers, M., Travis, N., Traiglio, J., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.,

Direct Submission, L., Zimmer, A. and Zody, M.,
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Mus musculus clone RP23-151C4, WORKING DRAFT SEQUENCE, 11 unordered
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Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-151C4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 193005;
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95.0%; Pred. No. 6.7e+02;
live 0; Mismatches 1;
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complement(41009. .41358)
                                                                                                                      /rpt family="Lx2"
complement (37781, .37846)
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37856 .37907
                                                                                                                                                                                                                       /rpt_family="(GAAAA)n"
37927. .39279
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complement (39361. .39633)
                                               complement (35586. .36658) /rpt_family="Lx2"
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40346. .40666
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HTG; HTGS PHASEI; HTGS DRAFT.
MUS mUSCULUS (house mouse)
Mus musculus
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complement (34807.
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Best Local Similarity 95.0°
Matches 19; Conservative
                                                                            /rpt_fa
36654.
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40699.
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RESULT 39
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                            Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Barten, B., Nusbaum, C., Lander, B., Camarata, J., Chang, J., Choepel, Y., Boughgalter, B., Camarata, J., Chang, J., Choepel, Y., Cook, A., Cooke, P., Corum, B., DeArellano, K., Colymore, A., Cook, P., Corum, B., DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B., Indblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Maratas, A., Karls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Macdonald, P., Major, J., Micol, R., Micol, R., Micol, R., Peterson, K., Phukhang, P., Pierre, N., Nell, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Rachupka, A., Ramasam, U., Reterson, K., Phukhang, P., Pierre, N., Talamas, J., Tedaners, J., Schubback, R., Sewary, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tedayers, T., Travers, M., Wassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Nu, X., Wassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Smit, A.F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/Repeatmasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contacts sequence submissions@genome.wi.mit.edu
Contert project Information
Center project name: 119755
Center clone name: 151 C 4
Center clone name: 152 C 4
Center clone name: 151 C 4
Sequencing vector: Plasmid; n/a; 100% of reads
Cequencing vector: Plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 19727 bases at least Q40
Consensus quality: 197965 bases at least Q40
Consensus quality: 198182 bases at least Q20
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Insert size: 198432; sum-of-contigs
Quality coverage: 9.1 in Q20 bases; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120838: contig of 8378 bp in Lengua
130838: gap of 100 bp
142226: contig of 11288 bp in length
142326: gap of 100 bp
159415: contig of 17089 bp in length
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gap of 100 bp
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Web site: http://www-seg.wi.mit.edu
(bases 1 to 199432)
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    REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (Dases 1 to 242301)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsebrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banka, T., Barbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Barka, T., Burbrooks, S.L., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Briewa, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.P., Carten, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACU10172 242301 bp DNA linear HTG 08-JAN-2003
Homo sapiens chromosome 12 clone RP11-551G13, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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159515: gap of 100 bp
197685: contig of 38170 bp in length
197786: gap of 100 bp
199432: contig of 1647 bp in length.
                                                                                                                                                                                                                                                      /clone_lib="RPCI-23 Female Mouse BAC"
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AC010172.21 GI:20279305
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
68.1%; Score 18.4; DB 2;
Best Local Similarity 95.0%; Pred. No. 6.7e+02;
Matches 19; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
122461. 130838
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130339. 142226
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142327. 159415
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159516. 197685
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197786. .199432
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                                                                                                      Location/Qualifiers
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soon as it is available and the accession number will
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/organism="Homo sapiens"
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144. .1283
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95321019
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Best Local Similarity 95.0
Matches 19; Conservative
                  as soon as it
be preserved.
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159930
160030
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3143
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6231
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AUTHORS
TITLE
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SOLEU2
LOCUS
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Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Gaucia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hanes, A., Hamilton, K., Harris, C., Harris, K., Harr, M., Havlak, P., Hawes, A., Hernandez, J., Harris, C., Harris, K., Harr, M., Havlak, P., Hawes, J., Jackson, L. B., Jacobson, B., Jia, Y., Johnson, R., Yolivet, S., Joudah, S., Karloson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Katovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Lucier, R., Luna, R., Martinez, E., Mahesbwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Mahesbwari, M., Mayuen, P., Martin, R., Martindale, A., Martinez, E., Moseer, M., Mei, G., Metzker, M., Mayuen, N., Nickerson, E., Novekenwo, S., Oguh, M., Okwonu, G., Oragunye, N., Oviedo, R., Parimus, E., Nwokenkwo, S., Oguh, M., Owiedo, R., Primus, E., Pu, L. L., Quiles, M., Rolas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scher, R., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stone, H., Saudez, L., Vara, S., Warren, Y., Thomas, S., Warren, R., Washington, C., Wallington, S., Walliams, G., Williams, G., Williams, A., Williams, C., Williams, C., Williams, S., Warren, R., Wooden, S., Worley, K., Warren, S., Le, C., Williams, S., Warren, R., Wooden, S., Worley, K., Weller, C., Marington, C., Walliams, C., Wallia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
Submitted (15-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 242301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-JAN-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 24, 2002 this sequence version replaced gi:14547712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-primer Bodipy: 46% of reads
Chemistry: Dye-terminator Big Dye: 54% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 234054 bases at least Q40
Consensus quality: 236536 bases at least Q30
Consensus quality: 238152 bases at least Q30
Estimated insert size: 250993; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...--- Summary Statistics
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Sequencing vector: M13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Unpublished
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JOURNAL
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AUTHORS
TITLE
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TITLE
JOURNAL
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COMMENT

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Iserentant,D. and Verachtert,H.
Cloning and sequencing of the LEU2 homologue gene of Schwanniomyces
occidentalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLN 25-APR-1995
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3-isopropylmalate dehydrogenase; LEU2 gene.
Debaryomyces occidentalis
Debaryomyces occidentalis
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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ISerentant, D.M.M.
Iserentant, D.M.M.
Subrission
Submitted (2-JUN-1994) D.M.M. Iserentant, University Leuven -
Iab., Ind. Microbiol. & Biochem., Kardinaal Mercierlaan 92, 3001
Heverlee, BELGIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 242301;
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3042: contig of 3042 bp in length
3142: gap of unknown length
6330: contig of 2988 bp in length
6430: gap of unknown length
14402: contig of 8172 bp in length
14502: gap of unknown length
31187: contig of 16685 bp in length
31287: gap of unknown length
525865: contig of 24578 bp in length
55865: gap of unknown length
78599: contig of 24578 bp in length
78699: gap of unknown length
108718: contig of 2634 bp in length
108718: contig of 261111 bp in length
159929: contig of 30019 bp in length
169029: gap of unknown length
169029: gap of unknown length
160029: gap of unknown length
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/mol_type="Genomic DNA"
/strain="ATCC26077,R91"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/protein_id="CAA56224.1"
/db_xref="G1:79113"
/db_xref="G1:79113
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ORIGIN

Query Match 67.4%; Score 18.2; DB 8; Length 1465; Best Local Similarity 87.0%; Pred. No. 5.5e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Search completed: January 7, 2005, 11:33:30 Job time: 938.789 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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model
3
using
search,
nucleic
1
OM nucleic

7, 2005, 10:58:39; Search time 205.579 Seconds (without alignments) 689.440 Million cell updates/sec January Run on:

US-09-786-502A-7 27

1 geggeegeaattgaagttatgtateet 27 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

8269772 Total number of hits satisfying chosen parameters: 4134886 segs, 2624710521 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* Geneseq 23Sep04:* geneseqn1980s:* geneseqn1990s:* Database

geneseqn2003cs:* geneseqn2003ds:* geneseqn2003as:* geneseqn2003bs:* geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

	Description	Aaa10270 Human CD2	Aba92024 Human CD2	Adl67231 Human CD2	Aat96357 CD28 cDNA	Ada02992 Human CD2	Adb72730 Human CD2	Adc85472 Human Cd2	Adm74587 Human car	Aag28837 Sequence	Aag21167 Human CD2	Human (Aat14707 Human CD2	Aav63445 Human CD2	Aav81203 Human CD2	Aaa50581 Human cel	Aaz29325 Human CD2	Aas03175 Human lym	Aba99035 Human CD2	Add25537 Binding d	Adi31990 Human cDN	Ado49343 Human CD2
SOMEWALES	ΩI	AAA10270	ABA92024	ADL67231	AAT96357	ADA02992	ADB72730	ADC85472	ADM74587	AAQ28837	AAQ21167	AAT36257	AAT14707	AAV63445	AAV81203	AAA50581	AAZ29325	AAS03175	ABA99035	ADD25537	ADI31990	AD049343
	DB	<u>_</u> س	9	12	~	σ	10	10	12	0	7	~	~	7	~	m	m	4	9	10	11	12
	Query Match Length DB	27	27	328	099	663	663	663	663	762	1514	1514	1514	1514	1514	1514	1514	1514	1514	1514	1514	1514
æ	Query Match	100.0	100.0	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4
	Score	27	27	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19
	Result No.	-	7	m	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21

Aas89399 DNA encod Aan90607 CD28 anti Aan49546 Human CD2 Ada02991 Human CD2 Ada02991 Human CD2 Adb72729 Human CD2 Adm74586 Human Car Adm0585 Antipsori Aad21976 Human CD2 Ada02990 Human CD2 Ada02990 Human CD2 Adc8470 Human CD2 Adc86406 Bacteriop	Aaa69168 Bacteriop Aah94213 Human foe Adj41623 Plant cDN Ab124354 Drosophil Acf6174 Photorhab Ab127568 Drosophil Continuation (6 of Continuation (7 of Continuation (9 of
MAMMA MA MA	AAA69168 AAH94213 AD41623 ABL24354 ACE68174 ABL27568 AAV21209_05 AAV21209_06 ACE67367_08
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	w n 12 4 13 4 4 4 4 13
1555 1555 1555 1555 1555 1555 1555 155	56506 392 2000 4093 4878 9265 110000 110000
7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	67.4 66.7 66.7 66.7 66.7 7.9 66.7 7.99
	18.2 18 18 18 18 18 18 18
00000000000000000000000000000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
U	U U

ALIGNMENTS

CD28; cytoplasmic domain; prostate-specific membrane antigen; PSWA; J591 hybridoma; monoclonal antibody; single chain variable region; scFv; single chain antibody; fusion receptor; immune response; prostate cancer; PCR primer; ss. Human CD28 fragment upstream PCR primer. AAA10270 standard; DNA; 27 BP. (first entry) 03-JUL-2000 AAA10270; RESULT 1 AAA10270

WO200014257-A1. Homo sapiens. 16-MAR-2000 99WO-US020349. 98US-0099138P. 03-SEP-1999; 04-SEP-1998; (SLOK) SLOAN KETTERING INST CANCER RES.

Ξ Gong Sadelain M, Bander NH,

WPI; 2000-257002/22.

A fusion receptor composition having the structure:prostate-specific membrane antigen-single chain variable fragment:optional connector:cytoplasmic domain, useful for treatment of cancer.

Example 6; Page 15; 25pp; English

The invention relates to a novel fusion receptor composition having the structure: PSMA (prostate-specific membrane antigen)-scFv (single chain variable fragment):optional connector:cytoplasmic domain, where the fusion receptor is effective when expressed in a T-cell to promote a cellular immune response to PSMA. The PSMA-scFv is a single-chain antibody cloned from the V region genes of a hybridoma specific for PSMA, such as J591. The optional connector is provided to give a spacing

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substantial function. The cytoplasmic domain, such that both retain substantial function. The cytoplasmic domain directs the function of the cusion receptor and is generally the cytoplasmic domain of a molecule which functions as a transducer of a mammalian immune response in the presence of an WHC (major histocompatibility complex)-peptide complex or costimulatory factor. Examples of cytoplasmic domains that may be employed in the present invention include the T-cell receptor gamma-chain cytoplasmic domain and the CD28 cytoplasmic domain. In a method of the invention, an expression vector encoding the fusion receptor is transduced into primary T-lymphocytes obtained from the patient to be treated. The transduced lymphocytes are returned to the patient to be treated. The transduced lymphocytes are returned to the patient to PSWA-colls. The fusion receptor function cytoplasmic and proliferate in response to PSWA-cells. The fusion receptor promotes a cellular immune response to PSWA and can thus be used to target PSWA-positive tumour cells. The treatment of prostate cancer and other cancers that express PSWA. Sequences AAA10270-A10271 represent PCR primers used in an exemplification of the present invention to amplify cDNA encoding the carrest content and content content content cancer and content cancer cancer and content cancer cancer and content cancer and content cancer cancer and content cancer cancer cancer and content cancer cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a gene encoding a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain of human CD28. This was used to construct a gene
receptor comprising the PSMA-scFv and the CD28 fragment
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Sequence 27 BP; 6 A; 6 C; 7 G; 8 T; 0 U; 0 Other;

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                                                  Gaps
                                                  .
Query Match
100.0%; Score 27; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 27; Conservative 0; Mismatches 0; Indels
                                                                                       1 GCGGCCGCAATTGAAGTTATGTATCCT 27
                                                                                                                            1 GCGCCGCAATTGAAGTTATGTATCCT 27
                                                                                       ò
                                                                                                                            셤
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ABA92024 standard; DNA; 27 BP (first entry) 23-MAY-2002 ABA92024; RESULT 2

Human CD28 cDNA upstream PCR primer.

CD28; T cell; receptor; human; antitumour; immunostimulant; cancer; therapy; neuroblastoma; melanoma; sarcoma; small lung carcinoma; brain tumour; disialoganglioside GD2; imaging; PCR; primer; ss.

Homo sapiens

US2002018783-A1.

14-FEB-2002.

97US-00940544. 30-SEP-1997; 97WO-US004427. 20-MAR-1997;

SADELAIN M. CHEUNG N V. KRAUSE A. GUO H. (SADE/) (COOH/) (CHEU/) (KRAU/)

Guo H; Krause A, Cheung NV, Sadelain M,

WPI; 2002-239251/29.

New fusion protein, useful for inducing host immune response, comprises variable region of light chain of an antibody linked to variable region of antibody, CD28 receptor signaling domain and transmembrane domain.

Example 3; Page 4; 9pp; English.

The present sequence is that of an upstream primer, used with the

downstream primer given in ABA92025, in the PCR amplification of a segment of human T cell surface receptor CD28 cDNA. The amplified segment encodes part of the extracellular domain of CD28, and the transmembrane and the cytoplasmic domains. Plasmid phosCD28 was used as template. The 5 primer contains a Bamid site, and these sites in the PCR product were used to facilitate insertion into retroviral vector SFG. A cell-surface molecule capable of CD28 signalling in T cells interacting with disialoganglioside GD2 tumours was signalling constructed. This comprised the antigen-binding site of a GD2-specific antibody and the transmembrane and signalling domains of the CD28 molecule. This is an example of fusion proteins of the invention comprising such fusion proteins exhibit enhanced survival when reintroduced to an in vivo environment. They can be used to induce an immune response to cells, particularly tumour cells which express the anti-GD2 sefv are useful for treatment and anti-GD2 sefv are useful for treatment of melanomas, and head to manned anti-GD2 sefv are useful for treatment of melanomas, and head to manned anti-GD2 sefv are useful for treatment of melanomas. neuroblastomas, small lung carcinoma, sarcomas and brain tumours that express GD2 as a surface antigen. Cells expressing the fusion proteins of the invention can also be used for in vitro purging of stem cells or bone marrow and for in vivo targeting of tumour cells and other antigenbearing cells for imaging

Sequence 27 BP; 6 A; 6 C; 7 G; 8 T; 0 U; 0 Other;

Gaps .. Score 27; DB 6; Length 27; Pred. No. 0.003; 0; Indels 0; Mismatches 100.0%; Query Match
Best Local Similarity 100...
-27, Conservative

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ADL67231 standard; DNA; 328 BP. 20-MAY-2004 (first entry) ADL67231; RESULT 3 ADL67231

Human CD28 costimulatory signalling element DNA.

T cell receptor; TCR; CD3 zeta chain; co-stimulatory signalling region; binding element; immunostimulant; therapy; cancer; human; ds.

Homo sapiens.

04-MAR-2004.

28-MAY-2003; 2003US-00448256.

28-MAY-2002; 2002US-0383872P.

(SLOK) SLOAN KETTERING INST CANCER RES.

Sadelain M, Brentjens R, Maher J;

WPI; 2004-225696/21.

New nucleic acid polymer encoding a chimeric T cell receptor having a zeta chain portion, useful for treating disorders where the immune response needs to be induced, such as cancer.

Example 7; SEQ ID NO 6; 25pp; English.

The invention relates to a nucleic acid polymer encoding a chimeric T cell receptor (TCR) which comprises human CD3 zete chain intracellular domain, a co-stimulatory signalling region and a binding element that specifically interacts with a selected target. The methods and

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RESULT 4

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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to crecombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising comprising cancer acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a blochip comprising CA nucleic acid or CA nucleic acid. The sequences of the invention were identified using concogenic retroviruses, which insert into the genome of the host organism or random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or carcinoma (especially breast cancer, prostate cancer, lymphoma or carcinoma fespecially breast cancer, prostate cancer, lymphoma or carcinoma cards, proteins and antibodies are also useful as therefore agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid present sequence of the printed specifically claimed human CA nucleic acid consequence of the invention. Note: The complete sequence data for this sequence of the invention. Note: The complete sequence data for this cancer and an according and evaluating drug candidates. The printed specification, but was obtained in alectronic format directly from MIPO at the printed specification, but was obtained consequence.
                                                                                                                                                           Human, carcinoma associated; oncogene; carcinoma; cancer; breast;
prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                  Human CD28 carcinoma associated coding sequence, SEQ ID NO:1510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 663; 42;
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1510; 245pp; English.
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Pred. No.
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ID ADB72730 standard; cDNA; 663

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AC ADB72730;

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DT 04-DEC-2003 (first entry)
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                                                                       06-NOV-2003 (first entry)
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-587068/55.
                                                                                                                                                                                                                                                                                                      WO2003057146-A2
                                                                                                                                                                                                                                                             Homo sapiens.
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                            ADA02992;
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compositions of the invention are useful for treating disorders where the immune response needs to be induced, such as cancer. The present sequence is human CD28 costimulatory signalling element DNA.
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B7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New xanthene derivatives useful as immunomodulators - e.g. methyl 2- (carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-methyl-9-oxo-9H-
                                                                                                                                                                                        Gaps.
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                                                                                                                                     Match 70.4%; Score 19; DB 12; Length 328; Local Similarity 100.0%; Pred. No. 37; les 19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening; inhibitor; enhancer; binding; CD28; B7-1; ds.
                                                                                             Seguence 328 BP; 75 A; 94 C; 77 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hida T, Hattori M, Kurokawa T, Nakanishi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 81; 117pp; English.
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ADA02992
ID ADA02992 standard; cDNA; 663 BP.
                                                                                                                                                                                                                                                        4 AATTGAAGTTATGTATCCT 22
                                                                                                                                                                                                                                                                                                                                                                                              AAT96357 standard; cDNA; 660 BP.
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96JP-00262085
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02-OCT-1996;
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The invention relates to new recombinant nucleic acids. The invention also relates to a host cell comprising a recombinant nucleic acid or expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, a cid, a recombinant protein,
                                                                                      New recombinant nucleic acid comprising a nucleotide sequence of any of
the carcinoma-associated (CA) genes, useful for screening for drug
candidates for diagnosing or treating carcinomas.
                                                                                                                                                                             The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rcinoma associated nucleic acid; CA nucleic acid; gene; de associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                                                                                                                                                                                                                                                                                                                   70.4%; Score 19; DB 10; Length 663; 100.0%; Pred. No. 42; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         Sequence 663 BP; 165 A; 168 C; 151 G; 179 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human carcinoma associated (CA) nucleic acid #129
                                                                                                                                                    Claim 1; SEQ ID NO 258; 983pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 258; 29pp; English.
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02-MAR-2001; 2001US-00798586.
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                              EK;
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Best Local Similarity 100.
Matches 19; Conservative
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(SAGR-) SAGRES DISCOVERY.
                              Engelhard
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                                                           WPI; 2003-513603/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic.
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                              Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; gene therapy, vaccine; cancer, carcinoma-associated gene; CA; secreted; transmembrane; intracellular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polymucleotide of the invention has oytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sarcomas. The present sequence represents a human cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                              cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                              neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00937722.
20-DEC-2001; 2001US-00034650.
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                                                                                                                                                                                     26-DEC-2001; 2001WO-US051291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                           Morris DW, Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Conservative
                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-239337/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                         WO2003008583-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003045230-A2
                 Human CD28 cDNA
                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-2004
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                                                                                                                                                      30-JAN-2003
                                            human; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC85472;
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                                                                cancer;
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ADC85472
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Soluble proteins binding to B7 proteins and block antigen presenting cells - are useful in treating T-cell mediated immunosuppression diseases e.g. transplant rejection, auto immune diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                       The CDNA sequence in AAQ28837 is derived from Aruffo A and Seed B, PNAS USA 84, 8573-77, 1987. The CD28 CDNA encodes a protein of 220 AAB (AAR27103). It contains a signal peptide from AAB 1-18 which is cleaved during the maturation of CD28 protein. The transmembrane region is AAB 153-79. For the production of soluble CD28 protein, the transmembrane region is CD28 protein to the protein is AAB region is deleted. The CD28 protein derived from P9-MIT comprises residues 19-157 and is not soluble. The CD28 protein derived from p9-CIT comprises residues 19-151 and is soluble. MIT and CIT are primers. Typiner is used as the 5' primer to pair with any 3' primer, eg. MIT and CIT, in a PCR reaction for the procurement of trucated CD28 gene which would direct the production of soluble CD28 protein. DNA encoding AAB 19-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 of CD28 is claimed. (Updated on 25-MAR-2003 to correct PN field.)
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100.0%; Pred. No. -r.,
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AATTGAAGTTATGTATCCT 27
             92WO-US001867,
                                                          91US-00666809
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Best Local Similarity 100.0
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                                                                                                                                                                                            WPI; 1992-331717/40.
                                                                                                    (CYTO-) CYTOMED INC
                                                                                                                                                                                                                    P-PSDB; AAR27103.
             09-MAR-1992;
                                                          08-MAR-1991;
                                                                                                                                                Ko J, Ip SH;
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21-MAY-1992
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carcinoma associated protein (CAP) encoded by a nucleotide sequence, a method of screening for a bioactive agent capable of modulating the activity of a CAP, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting the activity of a CAP, a method of treating carcinoma, a method for inhibiting the activity of a CAP, a method of treating carcinoma, a method of neutralising the effect of a CAP and a method of diagnosing carcinoma or propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a corcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the expression of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of more ganes comprising the nucleotide sequence in a first individual and comparing the expression of the gene from a second normal tissue type from the first individual or a second capacity of a CAP comprises from the first individual nor a second the first individual has carcinoma. A method of inhibiting the activity of a CAP comprises contracting an agent specific of or the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. The polypeptide specifically binds to the protein encoded by the nucleic acid. The nucleic acid. The comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acide are useful for proparing a composition for diagnosing or treating carcinoma e.g., brotein encoded by the nucleic acide the printed specification but was associated (CA) nucleic acide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was formed in electronic format directly from USPDO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 663 BP; 165 A; 168 C; 151 G; 179 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obtained in electronic format directly from USPTO at
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100.0%; Pred. No. -...
0; Mismatches
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/label= primer MIT
556. .570
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/label= primer ClT
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Best Local Similarity 100..
Loca 19; Conservative
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25-FEB-1993
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RESULT 9 AAQ28837

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Gaps

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DB 2; Length 762; 42; 0; Indels

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Antisense or triplex forming oligonucleotides which target sites within the present sequence, the CD28 cDNA, reduce T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host diseases, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning of cDNA encoding cell surface antigen - useful for isolation of diagnostic and therapeutic proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell surface antigen; cloning; immunoselection; immunotherapy; therapy; diagnosis; vector; piH3M; CD28; COS; T-lymphocyte; ss.
           Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1514; 47;
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                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                     70.4%; Sco...
100.0%; Pred. No...
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                                                                                       Disclosure, Fig 1B; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 AATTGAAGTTATGTATCCT 456
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89US-00379076.
90US-00553759.
92US-00983647.
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Best Local Similarity 100.
Matches 19, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CD28 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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30-OCT-1996
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AAT14707
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                                                                                                                                                                         A library of recombinants having inserts greater than 0.8kb in size was prepared in the piH3M vector (see AAQ21166) from 1 microgram of polyA (plus) RNA isolated from the human lymphoblastoid cell line JY. The library was screened from the buman lymphoblastoid cell line JY. The antibody enrichment method (see e.g. AAQ21164 or AAQ21165). After the third transfection, COS cells were panned with a specific anti-CD28 Ab. A Hirt supernatant was generated and transfected into E.coli. DNA was prepared from the resulting colonies and transfected into COS cells. Surface expression of CD28 antigen was detected in 3 of the 8 transfected cultures by indirect immunofluorescence. The CDNA insert from one of the positive clones was sequenced. (Updated on 25-MAR-2003 to correct PA
                                                                                       encoding it - for immuno-therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reduction, T cell, CD28, gene expression, treatment, immune system, disorder, graft versus host disease, septic shock; viral disease, pooriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis,
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 2; Length 1514;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systemic lupus erythematosus; inflammatory bowel disease;
triplex forming; antisense; oligonucleotide; ss.
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                                                                                     New CD53 cell surface antigen and DNA encoding and diagnosis of haematopoietic neoplasms, etc
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100. .762
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                                                                                                                                            Example 3; Fig 7; 160pp; English.
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95US-00529878
Aruffo A, Amiot M;
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(first entry)
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Matches 19; Conservative
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P-PSDB; AAW02131.
                                  WPI; 1992-056864/07
                                                   P-PSDB; AAR20805
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15-APR-1997
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Seed B,
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cDNAs from mammalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell. It has been used to clone genes (see AAV63442-63) encoding cell surface antigens associated with mammallan lymphocytes such as CD1-53, ICAM, LFA-3, FCRIA, FCRID, TLisA and Leu8 (see AAW80440-55). CD28 polypeptide (see AAW80442) has been expressed in transfected COS cells. The purified genes and proteins are useful for immunodiagnostic and immunotherapeutic applications, including the diagnostis and treatment of immune-mediated infections, diseases, and clasorders of animals, including humans. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell surface antigens, constructing cDNA libraries, expressing vectors for expression in eukaryotic cells or their fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell surface antigen; human; T cell antigen; T lymphocyte;
                                                                                                                                                                                                                                                                                                            70.4%; Score 19; DB 2; Length 1514; 100.0%; Pred. No. 47; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
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Allen J, Simmons D, Aruffo A;
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100. .153
/*tag= b
154. .759
/*tag= c
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Best Local Similarity 100.
Matches 19, Conservative
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Lauffer L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA library; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CD28 cDNA.
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01-DEC-1992;
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Amiot M,
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                                                        A cDNA clone (AAT14707) codes for human CD28 antigen (AAR91433). It was derived from human T-cell tumour library in COS cells using cDNA derived from human T-cell tumour line HPB-ALL and vector piH3M (see also AAT14705), and panning of the library using antibody-coated plates. This immunoselection cloning method, developed to clone genes for cell surface antigens of human lymphocytes (see also AAT14705-04 and AAT14706-26), has general appln. Cell surface are obtd. for diagnostic and therapeutic use. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This nucleotide sequence comprises human CD28 cDNA. The cDNA was isolated from HPB-ALL human T-cell tumour cells using a novel method for cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cloning vector and poly:linker - based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially human
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                           Score 19; DB 2; Length 1514;
Pred. No. 47;
                                                                                                                                                                                                                          Sequence 1514 BP; 404 A; 359 C; 337 G; 414 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                 0; Indels
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100.0%; Pred. No. ...
                        Example 3; Fig 7A-7B; 79pp; English.
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100. .762
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                        438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV63445 standard; cDNA; 1514 BP
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89US-00379076.
90US-00498809.
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92US-00983647
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100. .153
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(first entry)
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13-JUL-1989;
23-MAR-1990;
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07-JUN-1999
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AAV63445;

RESULT 13 AAV63445

Query Match Best Local S

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Matches

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Seed B,

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The present sequence is that of CDNA encoding human cell surface antigen (CSA) CD28 (see AAY96128). The CDNA was derived from a human T-cell tumour line HPB-ALL CDNA library using a new method for cloning CSA CDNAS. The method is based upon transient expression of CSA in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to (panning on) an antibody-coated substrate such as a culture dish. The predicted amino acid sequence of CD28 suggests an integral membrane protein with a single membrane-spanning hydrophobic domain terminating in a 41-amino acid cytoplasmic domain. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for immunodiagnostic and immunotherapeutic applications, including the disorders in animals, including humans. These disorders include asthma, immune-complex disease, amyloidosis, parasitic diseases or multiple
Isolated nucleic acid molecule encoding the CD19 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CD28; B7 molecule; immune response; cell surface receptor; Major histocompatibility complex; MHC classII; proton motor force; mitochondrial membrane potential; mitochondrial metabolism; cancer; autoimmune disease; neurodegenerative disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 3; Length 1514;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.4%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 47; Matches 19; Conservative 0; Mismatches
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/product= "Human CD28"
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                                                                                                                                          Example 3; Fig 7A-B; 75pp; English.
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98US-0094519P.
98US-0101580P.
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P-PSDB; AAY44294.
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29-JUL-1998;
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                                                    This nucleotide sequence comprises human CD28 CDNA. The CDNA was isolated from HPB-ALL human T-cell tumour cells using a novel method for cloning conformalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and physical calction of cells expression in eukaryotic cells and physical selection of cells expression for an antigen by adhesion to an antibody-contend substrate. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell: It has been used to clone genes contend to CD2, CD5, CD7, CD13, CD14, CD15, CD15, CD20, CD22, CD20, CD10, CD20, CD21, CD20, CD21, CD20, CD21, CD20, CD21, CD22, CD22, CD21, CD21, CD21, CD21, CD22, CD22, CD22, CD21, CD21, CD21, CD22, CD22, CD21, CD22, CD22,
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Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
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                   Example 3; Fig 7A-B; 79pp; English
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89US-00379076.
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Best Local Similarity 100.
Matches 19, Conservative
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P-PSDB; AAY96128.
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Gaps

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New recombinant DNA encoding CD28 useful for diagnosing and treating immune-mediated diseases, infections or disorders, e.g. systemic lupus erythematosus, asthma, transplant rejection, rheumatoid arthritis.

Example 3; Fig 7A-7B; 72pp; English

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Human lymphocyte cell surface antigen CD28 cDNA sequence.
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                             438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                            AAS03175 standard; cDNA; 1514 BP
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90US-00553759
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154. .759
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Best Local Similarity
Matches 19; Conserval
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                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  .3-JUL-1989;
                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                     17-APR-2001
                                                                                                                                                                                                        AAS03175;
                                                                                                                                                                                RESULT 17
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"CD28 antigen"

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The present sequence encodes human CD28 receptor. CD28 is a homodimeric glycoprotein involved in a secondary signalling pathway in the activation of T-cell proliferation. B7 on nerve cells can interact with CD28 on the immune cell leading to immune cell activation. The regulation of cell surface expression of MHC classII and co-stimulatory molecule B7 can be manipulated by regulating the intracellular dissipation of proton motor force which can be assessed in terms of mitochondrial membrane potential. These methods can be used for regulating cell growth and division to control disease processes by manipulating mitochondrial metabolism and the expression of cell surface immune proteins. They can be used for treating diseases associated with excessive cellular division, aberrant differentiation, and premature cellular death, e.g. cancers, autoimmune
of cell surface and membrane characteristics for developing products treating cancers, autoimmune diseases or neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 3; Length 1514;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 47; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases, neurodegenerative disorders etc
                                                                                                                                                                       Disclosure; Page 120-121; 123pp; English
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The present sequence encoding for numan lymphocyte cell surface antigen crossent sequence encoding the cobtain a new genetically engineered cDNA sequence encoding the CD28 amino acid extracellular domain sequence (amino acids 1 134 given in AA002437) and/or comprising nucleotides 100-759, 154-555 or 154-759 of the CD28 cDNA sequence. Various human lymphocyte cell surface antigen cDNA sequences (AA503172, AA503175-AA503195) are described in the present invention. The invention relates to a novel method of cloning cDNA encoding cell surface antigens and efficient construction of cDNA libraries. Also described are 2 expression vectors (AA503717, AA503174) which provide high level expression in eukaryotic host cells. The purified genes and proteins are useful for immunodiagnostic and immunotherapeutic applications, such as in the disonosts and treatment of immuno-mediated diseases, infections or disorders in animals and humans. Such diseases, infections or disorders and animals and humans. Such diseases include immune deficiency diseases of immediate type of hypersensitivity, asthma, hypersensitivity pneumonitis, systemic lupus erythematosus, rheumatoid arthritis, acute and chronic inflammation, platelet disorders, plasma and other cell neoplasms, parasitic diseases, multiple sclerosis, Guillain-Barre syndrome and tissue and organ transplant rejection. The sequences con also be used to identify, isolate and purify other antibodies and
                                                                                                                       sequence encoding for human lymphocyte cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; systemic sclerosis; dermatomyositis; polymyositis; Sjogren's syndrome; polyarteritis nodosa; vasculitis; sepsis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, CD28; immune response, T cell; graft-versus-host disease; GVHD; marrow transplant rejection; psoriasis; tissue transplant rejection; autoimmune disease; diabetes mellitus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 4; Length 1514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA99035 standard; DNA; 1514 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.48;
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu X, Anasetti C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YUXX/) YU X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-2002
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                                                                                                                       The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Gaps

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CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cycotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune
                                                                                                                                                                                                          The sequence represents the human CD28 gene. The invention relates to a novel method for inhibiting an immune response by administering an anti-cD28 antibody. The method of the invention has immunosuppressive, antipordatic, antidabetic, antiarthritic, antitheumatic, neuroprotective, dermatological, vasotropic, antiinflammatory, neuroprotective, dermatological, vasotropic, antiinflammatory, activity. The method works to inhibit immune response by reversing or blocking T cell activation. The method is useful for inhibiting an immune response in a subject susceptible to graft-versus-host disease (GVHD), marrow transplant rejection, or having autoimmune disease including psoriasis, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lupus erythematosus, systemic sclerosis, dermatomyositis, polymyositis, Sjogren's syndrome, polyarteritis nodosa or vasculitis. The method is also useful for treating sepsis, and other autoimmune diseases including autoimmune hepatitis, autoimmune haemolytic anaemia, Behcet's disease, myasthenia gravis, cirrhosis, uveitis, ulcerative colitis, and vitiligo
Inhibiting an immune response in a subject for treating autoimmune disease such as psoriasis, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, polymyositis, by administering anti-CD28 antibody.
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                                                                                                                                                         Disclosure; Page 28; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 AATTGAAGTTATGTATCCT 456
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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ADD25537
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New binding domain-immunoglobulin fusion protein, useful for treating a

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The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes detecting the hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes ocorrelates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a comparising a plurality of polymucleotide probes. The CDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polymucleotides. The microarray for monitoring
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.
subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene; 88; immunological response; immunopathological condition;
Crohn's disease; asthma; ulcerative colitis; hypereosinophilis;
irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
cutte monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                      70.4%; Score 19; DB 10; Length 1514; 100.0%; Pred. No. 47; cive 0; Mismatches 0; Indels (
                                                                                                                                       Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteopathic; antiarthritic; antirheumatic; cytostatic
                                                           Disclosure; SEQ ID NO 98; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1316; 50pp; English.
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                                                                                                                                                                                                                                                                                   438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                                                                                                                                                                                                                       ADI31990 standard; cDNA; 1514 BP.
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                                                                                                                                                                                            Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA #1316
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                                                                                                 Unidentified
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the diagnosis of an immunopathology, such as Crohn's disease, asthma, ulcerative colltis, hypereosinophilia, irritable bowel syndrome, osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forenics or pharmacogenomics. The composition may also be used in purification of asubpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell surface antigen; immune-mediated disorder; asthma; rheumatoid arthritis; multiple sclerosis; vasculitis; inflammation; ss;
                                                                                                                                                                                                                          Gaps
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                                                                                                                                       from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                   70.4%; Scor.
100.0%; Pred. No. -...
0; Mismatches
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                                                                                                                                                                                                                                                               438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                                                                                                                                                                                 ADO49343 standard; cDNA; 1514 BP
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90US-00498809.
90US-00553759.
92US-00983647.
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CD28 antigen cDNA
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ARUFFO A.
CAMBRINI D.
LAUFFER L.
OQUENDO C.
SIMMONS D.
STAMENKOVIC I.
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                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; human.
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01-DEC-1992;
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23-MAR-1990;
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(SIMM/)
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(ARUF/)
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                               The invention relates to a cloned cDNA segment encoding a cell surface antigen selected from CD1a, CD1a, CD1c, CD2, CD5, CD7, CD13, CD14, CD16, CD16, CD2, CD2, CD2, CD2, CD2, CD2, CD31, CD2w32a, CDw32b, CD31, CD34, CD36, CD37, CD38, CD39, CD4, CD3 and their functional derivatives. The cell surface antigens of human lymphocytes prepared from the CDNAs are useful in diagnosetic and therapeutic utility in immune-mediated disorders (aschma, rheumatoid arthritis, multiple sclerosis, vasculitis and inflammation) and infections in mammals, including humans. The present
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                DB 12; Length 1514; 47;
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                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                         sequence represents a human cell surface antigen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #25203.
                                                                                                                                                                                                                                                    70.4%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                 438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS89399 standard; cDNA; 1557 BP
Example 3; Fig 7; 75pp; English.
                                                                                                                                                                                                                                                                                                                                           9 AATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                  Local Similarity 100.
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P-PSDB; ABG25212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS89399;
                                                                                                                                                                                                                                                                    Query Match
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Revised record issued on 09-SEP-2004 : Correction to keywords

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polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed produces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyrosine suppressor gene; ASV LTR; human cytomegalovirus AD169 enhancer; HIV box; immunoselection; immune deficiency diseases; vasculitis; systemic lupus erythematosus; rheumatoid arthritis; neoplasms; ss.
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rapid immuno:selection cloning – used to clone genes encoding cell surface antigens associated with mammalian T lymphocytes.
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                                                                                                                                          Sequence 1557 BP; 392 A; 398 C; 361 G; 406 T; 0 U; 0 Other;
                                                                                                                                                                    5; Length 1557;
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                                                                                                                                                                            100.0%; Prea. ...
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Pred. No. 48;
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                                                                                                                                                                                                                                               193 AATTGAAGTTATGTATCCT 175
                                                                                                                                                                                                                                                                                                                       AAN90607 standard; cDNA; 1574 BP.
                                                                                                                                                                                                                         9 AATTGAAGTTATGTATCCT 27
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J, Stamenkovi I;
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                                                                                                                                                                     70.4%;
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100. .274
/*tag= b
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Best Local Similarity 100...
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD28 antigen cDNA.
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Unidentified
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31-OCT-2002
20-DEC-1989
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Simmons D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of therapeutically downmodulating an autoimmune response or an ongoing autoimmune response, comprising administering an antigen binding portion of an anti-CD28 antibody that blocks signaling via CD28 to the subject so that an autoimmune response or an ongoing autoimmune response in the subject is downmodulated. The methods are useful in therapeutically and downmodulated. The methods are useful in therapeutically and autoimmune disorders such as diabetes, allergy and allergic reactions, transplantation rejection, graft versus host disease, systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune thyroiditis, vitiligo, alopecia, inflammatory bowel disease, Addison's disease, Graves disease, haemolytic anaemia and Sjogren's syndrome. The present sequence is the human CD28 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Downmodulating immune responses by blocking CD28-mediated signaling, useful for preventing and/or treating autoimmune disorders such as diabetes, allergic reactions, graft versus host disease, systemic lupus
                                                                                                Gaps
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                              429 T; 0 U; 0 Other;
                                                              DB 1; Length 1574;
48;
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/product= "CD28"
/transl_except= (pos:867. .872,aa:Ala)
                                                   70.4%; Sco...
100.0%; Pred. No....
0; Mismatches
                              Sequence 1574 BP; 423 A; 375 C; 347 G;
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                                                                                                                                                                    498 AATTGAAGTTATGTATCCT 516
                                                                                                                                                                                                                                                        BP.
                                                                                                                                  27
                                                                                                                                  9 AATTGAAGTTATGTATCCT
                                                                                                                                                                                                                                                      AAL49546 standard; DNA; 3803
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                                              Query Match
Best Local Similarity luv.v.
Best 19; Conservative
                                                                                                                                                                                                                                                                                                                                                             Human CD28 coding sequence.
                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell; cell proliferation; cell survival; cytostatic; antiallergic; immunostimulant; immunosuppressive; gene therapy; CD28; human; gene; ds.
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                                                                                                                                 Gaps
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Sequence 3803 BP; 1076 A; 766 C; 880 G; 1081 T; 0 U; 0 Other;
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                                                             6; Length 3803;
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                                                                                                                                 0; Indels
                                     70.4%; Scor.
100.0%; Pred. No. 5.,
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223. .885
/*tag= a
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/product= "CD28"
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                       Query Match
Query Match
Best Local Similarity 100.00
Change 19; Conservative
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ABV77531
ABV775351
ABV77531
ABV77
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a cinvention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a blochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism or transported host norogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host correctionma (especially breast cancer, prostate cancer, lymphoma or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as the sequence represents as specifically claimed human CA nucleic acid present sequence are specifically claimed human CA nucleic acid sequences or present sequence represents as specifically claimed human CA nucleic acid specially claimed human CA nucleic acid and antibodies are also useful as the sequence represents as specifically claimed human CA nucleic acid
                                                                                                                                                                                                                                                                                                                                Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic formst directly from WIPO at
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                                                                                                                                                                                                                                                                                    Human CD28 carcinoma associated cDNA, SEQ ID NO:1509.
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                         561 AATTGAAGTTATGTATCCT 579
                                                                                                                                                    ADA02991 standard; cDNA; 3804 BP
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9 AATTGAAGTTATGTATCCT
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             gene; ss.
                                                                                                                                                                                                ADA02991;
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                                                                                                           RESULT 2
ADA02991
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Gaps ; 0

0; Indels

70.4%; Score 19; DB 8; Length 3804; 100.0%; Pred. No. 55;

ilarity 100.0%; Pred. No. 55; Conservative 0; Mismatches

Query Match Best Local Similarity Matches 19; Conserva

ADB72729

RESULT 27

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New recombinant nucleic acid comprising a nucleotide sequence of any of
the carcinoma-associated (CA) genes, useful for screening for drug
candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, carcinoma associated nucleic acid, CA nucleic acid, gene; ss, carcinoma associated protein, CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New carcinoma associated gene or protein, useful for preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3804;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human carcinoma associated (CA) nucleic acid #128.
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                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 257; 983pp; English
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02-MAR-2001; 2001US-00798586.
                                                                                            12-DEC-2002; 2002WO-US038582.
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                                                                                                                                                                         (SAGR-) SAGRES DISCOVERY
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(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                             Morris DW, Engelhard
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                                                                                                                                                                                                                                                  WPI; 2003-513603/48.
                  WO2003045230-A2
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                                                      05-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
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                                                                                                                                                                                                                                  human; ss; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma.
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Pred. No.
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                                                                            ADB72729 standard; mRNA; 3804 BP
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100.0%;
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23-CCT-2001, 2001US-00004113.
08-NOV-2001, 2001US-00052482.
30-NOV-2001, 2001US-00937722.
20-DEC-2001, 2001US-00034650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Engelhard EK;
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Best Local Similarity
Lag 19; Conserva
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                                                                                                                                                                                               Human CD28 mRNA
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ADC85471;

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Gaps

The invention

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carcinoma associated protein amethod of screening for drug candidates, a card, a recombinant nucleic acid or expression vector comprising a recombinant nucleic card, a method of screening for drug candidates, a method of screening for a bioactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a method of screening for a bioactive agent capable of modulating the activity of a CAP, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method of inhibiting the activity of a CAP, a method of treating carcinoma, a method of cardinoma or propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a corrinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the mucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of the gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of the gene from the patient the first individual and comparing the expression of the gene from or an encomparing the nucleotide sequence. A second normal tissue type from the first individual and comparing the expression of the gene from the first individual and comparing the expression of the gene from the first individual and comparing the expression indicates that the first individual and comparing the expression of the gene carcinomas comprises administering to a patient an inhibitor of CAP. Treating carcinomas comprises administering to a patient an inhibitor of CAP. Treating carcinomas comprises administering to a patient an inhibitor of CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the polypeptide specification or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparing a composition for diagnosing or treating carcinoma e.g., leukaemia or lymphoma. This sequence represents a human carcinoma associated (CA) nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
composition for diagnosing or treating carcinoma e.g., leukemia or
lymphoma.
                                                                                                                                                                                             The invention relates to new recombinant nucleic acids.
                                                                                                                         Claim 1; SEQ ID NO 257; 29pp; English
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Les 19; Conservative
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Matches
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Gaps ö Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other; 70.4%; Score 19; DB 12; Length 3804; 100.0%; Pred. No. 55; ive 0; Mismatches 0; Indels

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ADN05855 standard; cDNA; 3804 BP 01-JUL-2004 ADN05855 RESULT 30 ADN05855

Antipsoriatic cDNA sequence #1159 (first entry)

ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.

Homo sapiens.

08-APR-2004.

WO2004028479-A2

25-SEP-2003; 2003WO-US030907

25-SEP-2002; 2002US-0414006P

New construct for downmodulating immune response in a subject, has exposed surface attached with antigen-binding portion of antibody that binds to cytotoxic T lymphocyte antigen-4 and major histocompatibility molecule.

Kranz

Griffin M,

Whitters M,

Collins M,

Bluestone JA,

WPI; 2002-017603/02.

P-PSDB; AAE13721.

(GETH) GENENTECH INC

ö Human, cytotoxic T lymphocyte antigen-4; CTLA-4; CD28; AIDS; therapy; Acquired Immune Deficiency Syndrome; neuroprotective; dermatological; immune response; organ transplantation; autoimmune disease; allergy; SLE; systemic lupus erythematosus; multiple sclerosis; tumour vaccination; immunodeficiency disease; DiGeorge Syndrome; cancer; ds. The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention. Wood WI; Gaps New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in ö Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other; DB 12; Length 3804; 55; Schoenfeld J, Williams PM, Indels . 0 /product= "Human CD28 protein" Query Match 70.4%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 55; Matches 19; Conservative 0; Mismatches Claim 1; SEQ ID NO 2250; 3069pp; English. cocation/Qualifiers Jackman J, 86 9 AATTGAAGTTATGTATCCT 27 AAD21976 standard; DNA; 3806 12-APR-2001; 2001WO-US012275 12-APR-2000; 2000US-0196851P. (first entry) 223. .885 (GEMY) GENETICS INST INC. WPI; 2004-305105/28. P-PSDB; ADN05856. Clark H, Human CD28 DNA WO200179300-A1 sapiens 12-FEB-2002 25-OCT-2001. Bodary S, AAD21976; mammal, Wu TD Ношо RESULT 31 Key AAD2197 요 ઠ

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invention also encompasses expression vectors and host cells comprising
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                                                                                          The invention relates to a construct for downmodulating immune response in a subject. The construct comprises an exposed surface attached with an antighor binding portion of an antibody that binds to a cytotoxic T lymphocytic antigen (CTLA)-4 or CD28 expressed on T-cell of the subject, and a major histocompatibility complex (MMC) molecule. The construct is useful for treating an individual afflicted with a disease or disorder that would benefit from downregulation of immune response. Downmodulation of the immune response is useful to downmodulate the immune response in suscinct is useful to downmodulate the immune response in autoimmune diseases such as systemic lupus erythematosus and multiple sclerosis. The construct is useful for inhibiting immune call activation and prevents production of autoantibodies or cytokines which may be involved in disease such as systemic lupus erythematosus call activation is useful in the treatment of allergy and allergic reactions ery by inhibiting IgE production. The construct is also useful for enhancing desirable immune response in a subject e.g., in situations of tunour vaccination, in viral immunity or in immunodeficiancy diseases such as AIDS and Digeorge Syndrome. Induction/chanacement of immune cell function results in increased tumour destruction in cancer patients. The construct is also useful in treating infectious diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, carcinoma associated, oncogene, carcinoma, cancer, breast, prostate, lymphoma, leukaemia, cytostatic, gene therapy, drug screening;
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Disclosure; Page 93-94; 98pp; English.
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ADA02990
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The

New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

WPI; 2003-587068/55.

Morris DW;

Claim 1; SEQ ID NO 1508; 245pp; English.

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CA nucleic acid, a polypepting tensor, and antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using concogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acid, protein and antibodies are also useful as thereapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed human CA nucleic acid sequence of the invention. Note: The complete sequence data for this cancer in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid, useful for treating carcinomas, lymphomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51365 BP; 15176 A; 10059 C; 10474 G; 15656 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.4%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 82; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 556; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30447 AATTGAAGTTATGTATCCT 30465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB72728 standard; DNA; 51365 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2001; 2001US-00798586.
23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2001; 2001WO-US051291.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-239337/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CD28 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003008583-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 33
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Human, carcinoma associated nucleic acid; CA nucleic acid; gene; de carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;

Human carcinoma associated (CA) nucleic acid #127

(first entry)

01-JUL-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequence selected from any of the fully defined carcinoma-
associated (CA) genes from the 50 tables given in the specification. The
CA proteins are secreted, transmembrane or intracellular proteins. The
recombinant nucleic acids are useful for screening for drug candidates
for diagnosing or treating carcinomas. Sequences given in ADC85215-
ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; gene therapy, vaccine; cancer; carcinoma-associated gene; CA; secreted; transmembrane; intracellular; ds.
recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51365 BP; 15176 A; 10059 C; 10474 G; 15656 T; 0 U; 0 Other;
                                                                      Sequence 51365 BP; 15176 A; 10059 C; 10474 G; 15656 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid comprising a nucleotide sequence of ar
the carcinoma-associated (CA) genes, useful for screening for drug
candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant nucleic acid comprising a
                                                                                                                                            ö
                                                                                                    Query Match 70.4%; Score 19; DB 10; Length 51365; Best Local Similarity 100.0%; Pred. No. 82; Matches 19; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 256; 983pp; English.
                                                                                                                                                                                                  30447 AATTGAAGTTATGTATCCT 30465
                                                                                                                                                                                                                                                                                                        ADC85470 standard; DNA; 51365 BP.
                                                                                                                                                                                9 AATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-2002; 2002WO-US038582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-2001; 2001US-00997722
                                                                                                                                                                                                                                                                                                                                                                                                                Human Cd28 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morris DW, Engelhard EK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-513603/48.
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                                                                                                                                                                                                                                                                                                                                           ADC85470;
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New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia c

02-MAR-2001; 2001US-00798586.

(MORR/) MORRIS D

Morris DW, Engelhard EK; ENGE/) ENGELHARD E K.

WPI; 2004-328562/30

.ymphoma.

30-NOV-2001; 2001US-00997722. 22-DEC-2000; 2000US-00747377

US2004072154-A1. Homo sapiens.

cytostatic.

15-APR-2004.

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Line invention to tractes to law tecompliand indicate acid or expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, a method of screening for a bioactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma drug, a method of diagnosing carcinoma, a method of carcinoma drug, a method of diagnosing carcinoma, a method of carcinoma or carcinoma drug, a method of diagnosing carcinoma or propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of carcinoma cativation of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of comparing the first individual and comparing the expression of the gene comprises of a first individual and comparing the expression of the gene comprises diditional, where a difference in the expression indicates that the first individual has carcinoma. A method of inhibiting the activity of a CAP comprises contracting an agent specific content of the protein encoded by the protein encoded by the nucleic acid. It comprises an activation of the protein encoded by the nucleic acid, it comprises an activation of a protein encoded by the nucleic acid. The nucleic acid are nucleic acid. It comprises an activation of a carcinoma comparities and intended acid. The nucleic acid is are useful for the comparities and acid. The nucleic acid are nucleic acid. It comprises an acid. The nucleic acid are nucleic acid. The nucleic acid are nucleic acid. The nucleic acid are 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preparing a composition for diagnosing or treating carcinoma e.g., leukaemia or lymphoma. This sequence represents a human carcinoma associated (CA) nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to new recombinant nucleic acids. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51365 BP; 15176 A; 10059 C; 10474 G; 15656 T; 0 U; 0 Other;
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Gaps

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Indels

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70.4%; Score 19; DB 12; Length 51365; 100.0%; Pred. No. 82;

Best Local Similarity 100.0%; Pred. No. 82; Matches 19; Conservative 0; Mismatches

Query Match

Gaps

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0; Indels

100.0%; Prec. ...

Local Similarity 100. Les 19; Conservative

Matches

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30447 AATTGAAGTTATGTATCCT 30465

9 AATTGAAGTTATGTATCCT 27

ADM74585 standard; DNA; 51365 BP.

RESULT 35 ADM74585 ID ADM74 XX

Score 19; DB 10; Length 51365;

70.4%;

Query Match

(first entry)

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The present invention describes a method for identifying a bacteriophage coding region encoding a product active on an essential bacterial target. The method comprises identifying a nucleic acid sequence encoding a gene product that provides a bacteria-inhibiting function when an uncharacterised bacteriophage infects a pathogenic bacterium. The compound active on a target of a bacteriophage inhibitor protein in a bacterial is used to treat or prevent a bacterial infection in an animal. AAA68431 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage nucleotide and protein sequences which are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a bacteriophage coding region for treating bacterial infections comprises identifying a nucleic acid encoding a product that inhibits bacteria when a bacteriophage infects a bacterium.
                                                                                    Bacteriophage; antimicrobial; genome; identification; antibacterial; bacterial growth inhibition; bacterial infection; ds.
                                                            Bacteriophage Dp-1 complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Page 348-358; 456pp; English
                                                                                                                                                                                                                                                                                                                                                                     (PHAG-) PHAGETECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                  Pelletier J, Gros P,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-412361/35.
                                                                                                                                       Bacteriophage Dp-1.
                                                                                                                                                                  WO200032825-A2.
                                                                                                                                                                                                                               03-DEC-1999;
                              27-OCT-2000
                                                                                                                                                                                                                                                                                                                                       02-DEC-1999;
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                                                                                                                                                                                                 08-JUN-2000
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AAA69168;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for identifying a bacteriophage coding region encoding a product active on an essential bacterial target. The method comprises identifying a nucleic acid sequence encoding a gene product that provides a bacteria-inhibiting function when an uncharacterised bacteriophage infects a pathogenic bacterium. The compound active on a target of a bacteriophage inhibitor protein in a bacteria is used to treat or prevent a bacterial infection in an animal. AAA68243 to AAA69442 and AABI6553 to AABI6554 represent bacteriophage nucleotide and protein sequences which are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a bacteriophage coding region for treating bacterial infections comprises identifying a nucleic acid encoding a product that inhibits bacteria when a bacteriophage infects a bacterium.
                                                                                                                                                                                                                                          Bacteriophage; antimicrobial; genome; identification; antibacterial; bacterial growth inhibition; bacterial infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match
Local Similarity 87.0%; Pred. No. 1.38+02;
les 20; Conservative 0; Mismatches 3. 7-2-1-
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                                                                                                                                                                                                               Bacteriophage Dp-1 nucleotide sequence dp1ORF001.
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                               30447 AATTGAAGTTATGTATCCT 30465
              27
                                                                                                                      BP.
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99US-00407804.
99US-0157218P.
                                                                                                                      standard; DNA; 3692
                                                                                                                                                                                                                                                                                                                                                                                                                98US-0110992P
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99US-00454252
                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PHAG-) PHAGETECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the present invention
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                                                                                                                                                                                                                                                                                         Bacteriophage Dp-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAB16682
                                                                                                                                                                                                                                                                                                                       WO200032825-A2
                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1999;
28-SEP-1999;
30-SEP-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pelletier J,
                                                                                                                                                                                 27-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1998
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                                                                                                                                                    AAA69169;
                                                                                                                      AAA69169
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                                                                                       RESULT 36
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Dubow M;

98US-0110992P. 99US-00326144. 99US-00407804. 99US-0157218P. 99US-0168777P.

99US-00454252

99WO-IB002040

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; noctropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder; network system disorder; inflammation; expressed sequence tag; EST; ss.
                                                                                                                                 Gaps
                                        Sequence 56506 BP; 18170 A; 10773 C; 12019 G; 15544 T; 0 U; 0 Other;
                                                                                                                               ;
0
                                                                             Match 67.4%; Score 18.2; DB 3; Length 56506; Local Similarity 87.0%; Pred. No. 2.1e+02; les 20; Conservative 0; Mismatches 3: Indel8 0:
                                                                                                                                                                                                                     38279 GCCGCAACTGAAGTCATGTATGC 38301
                                                                                                                                                                            4 GCCGCAATTGAAGTTATGTATCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human foetal cDNA, SEQ ID NO: 742.
                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                                                                              AAH94213 standard; cDNA; 392
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
the present invention
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Gaps

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1582 GCCGCAACTGAAGTCATGTATGC 1604 GCCGCAATTGAAGTTATGTATCC 26

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Best Loc Matches

AAA69168 standard; DNA; 56506 BP

RESULT 37
AAA69168
ID AAA69

Glazebrook J;

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The invention relates to plant nucleotide sequences that direct seed, cleaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sumflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, cordum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to oiler improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or improve incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high mutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the plants of patent did not form part of the plante of patent did not form part of the plante of patent did not form part of the sequence data for this.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genomic polynucleotide SEQ ID NO 24535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2000 BP; 491 A; 502 C; 447 G; 559 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 66.7%; Score 18; DB 12; Length 20
Local Similarity 80.8%; Pred. No. 1.5e+02;
Les 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moughamer T, Briggs SP, Cooper B, Glaze
tagiri F, Kreps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1484 GCAGCCGCATTCGAAGGTGTGTATCC 1509
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26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                           BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
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                                                                                                                                                                                                                                                                                                                     KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                   KREPS J.
PROVART N.
                                                                                                                                                                                                                                                                                          GOFF S A.
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(ZHUT/) ;
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(GLAZ/)
(GOFF/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel foetal polypeptides encoded by polymucleotides comprising one of 477 sequences fully defined in the specification. The foetal polymucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, as yestem disorders and inflammation. The present sequence was assembled using an expressed sequence tag (EST) found to be expressed in human foetal tissue cDNA libraries as the seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boyle BJ, Arterburn MC,
Zhou P, Werhman T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 CTGCTGCAATTCAAGTTATTTCTCCT 138
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                                                                                                                                                                                                                                                                                    25-JAN-2000; 2000US-00491404.
15-SEP-2000; 2000US-00663870.
06-NOV-2000; 2000US-00707351.
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                                                                                                                                                                                                                           25-JAN-2001; 2001WO-US002723
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P-PSDB; AAM06538.
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Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                             WO200155339-A2
                                    Homo sapiens.
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Length 2000;

WO200171042-A2.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA acquences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 24535; 21pp + Sequence Listing; English.
                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                  Li PWD,
                                                                                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                      23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                 WPI; 2001-656860/75
                                                                                                                                                              (PEKE ) PE CORP NY.
                                  27-SEP-2001.
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Gaps ö Sequence 4093 BP; 1185 A; 920 C; 888 G; 1100 T; 0 U; 0 Other; Query Match 66.7%; Score 18; DB 4; Length 4093; Best Local Similarity 80.8%; Pred. No. 1.7e+02; Matches 21; Conservative 0; Mismatches 5; Indels

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Search completed: January 7, 2005, 11:40:47 Job time : 209.579 secs

Sequence Sequence

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Sequence

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Sequence Sequence

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GENERAL INFORMATION:
APPLICANT: Teuneaki HIDA et al.
TITLE OF INVENTION: XANTHENE DERIVATIVES, THEIR PRODUCTION AND TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: Washington
CITY: Washington
STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.4%; Score 19; DB 3; Length 660; 100.0%; Pred. No. 5.2; ive 0; Mismatches 0; Indels
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US-09-475-515-47
US-09-475-515-43
US-09-475-515-43
US-09-475-515-43
US-09-475-515-46
US-09-475-515-36
US-09-475-515-39
US-09-475-515-45
US-09-475-515-42
US-09-476-476-47-618-45
US-09-476-476-47-618-45
US-09-248-796A-5314
US-09-248-796A-5314
US-09-248-796A-5314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08812946A
Patent No. 6221637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 19; Conservative
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Sequence 1, Appli
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Sequence 1316, Ap
                                                                                                                 7, 2005, 10:58:39; Search time 48.7895 Seconds (without alignments) 393.349 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 US-09-692-570-1

US-09-107-532A-2735

US-09-702-498A-3

US-09-702-498A-3

US-09-702-498A-3

US-09-702-498A-3

US-09-702-498A-3

US-09-702-498A-3

US-09-702-498A-3

US-09-702-498A-3

US-09-536-977-13

US-08-536-977-43

US-09-536-977-47

US-09-536-977-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-812-946A-1
US-09-023-655-1316
US-08-916-421B-1
                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-324-243-34
-08-532-390-34
                                                                                                                                                                                                                    1 geggeegeaattgaagttatgtateet 27
                                                                                                                                                                                                                                                                                                 824507 seqs, 355394441 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                            US-09-786-502A-7
27
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Match Length DB
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1664976
2040
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                                                                                                                    January
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                                                                                   OM nucleic -
                                                                                                                                                                                                                        Sequence:
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                                                                                                                    Run on:
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or
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    CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INPORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INPORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: nequals a, t, c,
                                                                                                                                                                TYPE: DNA ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                           NAME/KSY: misc feature
LOCATION: (28222)
LOCATION: (28222)
NAME/KSY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (163385)...(163385)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (191989)...(191989)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (191995)...(191995)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (231980)...(231980)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (231980)...(231980)
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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LCCATION: (234187).. (234187)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (98120) (98120)
OTHER INFORMATION: n equals
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Sequence 1, Application US/08916421B
Fatent No. 6503729
GENERAL INFORMATION:
FALSEL INFORMATION:
FAILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
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                                                                                                        Sequence 1316, Application US/09023655
; Patent No. 6607970;
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY FAGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERRENCS/OCKET NUMBER: PA-0001 US
TELECAMUNICATION INFORMATION:
TELECHONE: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1316:
SEQUENCE CHARACTERISTICS:
339 AATTGAAGTTATGTATCCT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1514 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: GENBANK
CLONE: 9338444
US-09-023-655-1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-916-421B-1
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c, or g NAME/KEY: misc feature
LOCATION: (622708) .. (622708)

NAME/KEY: misc feature
LOCATION: (65708) .. (657081)

LOCATION: (657081) .. (657081)

OTHER INFORWATION: n equals a, t, c, or ö ö ö ö t, c, or c, or AME/KEY: misc feature OCATION: (779455)..(779455) THER INFORMATION: n equals a, t, c, AAME/KEY: misc feature LOCATION: (312837)..(312837) DIHER INFORMATION: n equals a, t, c, AME/KEY: misc feature OCATION: (779676)..(779676) VTHER INFORMATION: n equals a, t, c, JOCATION: (1084830)...(1084830)
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature
LOCATION: (1096846)...(1096846)
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature
LOCATION: (1119881)...(1119881)
OTHER INFORMATION: n equals a, t, c, misc, feature LOCATION: (1310988)...(1310988)
OTHER INFORMATION: n equals a, t, c, NAME/KYS: misc_feature
LOCATION: (1313224)...(1313224)
OTHER INFORMATION: n equals a, t, c, NAME/KYS: misc_feature
LOCATION: (1349473)...(1349473)
OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc_feature NAME/KEY: misc feature COCATION: (677203) .. (657203) 27HER INFORMATION: n equals a, t, NAME/KEY: misc feature COCATION: (674435) .. (674435) ION: (871619)..(871619) INFORMATION: n equals a, t, KEY: misc feature ION: (1130881)..(1130881) INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (31293).. (31293)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (319226).. (319226)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (559241)..(559241) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (600992)..(600992) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (682442) CTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (713522)...(713522) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (741684)...(741684) OTHER INFORMATION: n equals a, t, COCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, AME/KEY: misc_feature NAME/KEY: misc feature LOCATION: (559167). (559167) OTHER INFORMATION: n equals a, 'KEY: misc_feature KEY: misc feature KEY: misc_feature

ô Gaps ö Query Match 66.7%; Score 18; DB 4; Length 1664976; Best Local Similarity 80.8%; Pred. No. 78; Matches 21; Conservative 0; Mismatches 5; Indels 0; 609314 GCAGCAGCTATTGATGATATGTATCC 609339 1 GCGCCCCAATTGAAGTTATGTATCC 26 g ઠે

GENERAL INFORMATION:
APPLICANT: Bult et al.
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc Percent No. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: P827561
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 1996-08-12
PRIOR APPLICATION NUMBER: US 06/024,428
PRIOR APPLICATION NUMBER: US 08/316,421
PRIOR APPLICATION NUMBER: US 08/316,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH 1664976 RESULT 4 18-09-692-570-1 'Sequence 1, Application US/09692570 ; Patent No. 6797466

占 TYPE: DNA
ORGANISM: Methanococcus jannaschii
FRATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(38222)
OTHER INFORMATION: n equals a, t, c NAME/KEY: misc feature LOCATION: (84773)..(84773) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (28257)...(28258) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (84808)..(84808) OTHER INFORMATION: n equals FEATURE:

NAME/KEY: misc feature LOCATION: (84812)..(84812) OTHER INFORMATION: n equals a, t, c,

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FEATURE: NAME/KEY: misc feature LOCATION: (98120)(98120) OTHER UNFORMATION: n equals a,	NAME/KEY: misc feature LOCATION: (98159)(98159) OTHER INFORMATION: n equals a,	FEATURE NAME/KEY: misc feature LOCATION: (98239) (98239) OTHER INFORMATION: n equals a, FEATURE.	NAME/KEY: misc feature LOCATION: (98266)(98266) OTHER INFORMATION: n equals a,	misc featur (98343)(9 RMATION: n	FALUKEY: misc feature LOCATION: (103998)(103998) OTHER INFORMATION: n equals a,	FALVEY: NAME/KEY: misc feature LOCATION: (148948)(148948) OTHER INFORMATION: n equals a,	NAME/KEY: misc feature LOCATION: (163385)(163385) OTHER INFORMATION: n equals a,	FABATOKE: NAME/KEY: misc feature LOCATION: (191989)(191989) OTHER INFORMATION: n equals a,	misc (19: ORMA:	FALUE KENTER MISC FEATURE LOCATION: (231980). (231980). OTHER INFORMATION: n equals a,	FALUKEY: misc feature LOCATION: (234187)(234187) OTHER INFORMATION: n equals a,	FALUEY KEY: misc feature LOCATION: (234220) COTHER INFORMATION: n equals a,	FALUKE: NAME/KEY: misc feature LOCATION: (234814)(234814) OTHER INFORMATION: n equals a,	FALUKY: misc feature LOCATION: (309398)(309398) OTHER INFORMATION: n equals a,	FALUKE: NAME/KEY: misc feature LOCATION: (309418)(309418) OTHER INFORMATION: n equals a,	FALUKE: NAME/KEY: misc feature LOCATION: (312837)(312837) GTHER INFORMATION: n equals a,	NAME/KEY: misc feature LOCATION: (312993)(312993) OTHER INFORMATION: n equals a, FEATURE:

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NAME/KEY: misc feature
LOCATION: (559167)
OTHER INFORMATION: n equals a, t, c, or
FEATURE:
NAME/KEY: misc feature
LOCATION: (559241)
OTHER INFORMATION: n equals a, t, c, or
FEATURE:
NAME/KEY: misc feature
LOCATION: (600992)
OTHER INFORMATION: n equals a, t, c, or
FEATURE:
NAME/KEY: misc feature
LOCATION: (600992)
OTHER INFORMATION: n equals a, t, c, or
FEATURE:
NAME/KEY: misc feature
LOCATION: (600902)
OTHER INFORMATION: n equals a, t, c, or
OTHER INFORMATION: n equals a, t, c, or FEATURE:
NAME/KEY: misc feature
LOCATION: (1119881)
OTHER INFORMATION: n equals a, t, c,
FEATURE:
NAME/KEY: misc_feature ບັ ΰ ΰ ΰ ບັ ϋ OTHER INFORMATION: n equals a, t, c, PRATURE:
NAME/KEY: misc_feature
LOCATION: (779676)...(779676)
OTHER INFORMATION: n equals a, t, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (1084830)
OTHER INFORMATION: n equals a, t, c, FRATURE:
NAME/KEY: misc_feature
LOCATION: (1084830)
OTHER INFORMATION: n equals a, t, c, FRATURE:
LOCATION: (1084830)
OTHER INFORMATION: n equals a, t, c, CATHER INFORMATION: n equals a, t, c, CTHER INFORMATION: n equals a, t, c, CATHER INFORMATION: n equals a, t, c, CTHER INFORMATION: n equals a, t, c, CTHER INFORMATION: n equals a, t, c, CTHER INFORMATION: n equals a, t, c, ú FEATURE:
NAME/KEY: misc feature
LOCATION: (657081)...(657081)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc_feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t,
FEATURE:
LOCATION: (674435)..(67435)
OTHER INFORMATION: n equals a, t,
FEATURE:
LOCATION: (68242)..(682442)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc_feature
LOCATION: (68242)..(682442)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc_feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc_feature
LOCATION: (713654)..(713654)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc_feature
LOCATION: (714684)
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature LOCATION: (319226)..(319226) OTHER INFORMATION: n equals a,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Artificially synthesized sequence derived from the
                                                                                                                                                              Gaps
                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hasegawa, Mamoru
APPLICANT: Hasegawa, Mamoru
APPLICANT: Nagai, Yoshiyuki
ITILE OF INVENTION: Paramyxovirus vectors used for transfer
ITILE OF INVENTION: Of foreign genes
ITILE REPERENCE: 50026/025001
CURRENT APPLICATION NUMBER: US/09/702,498A
CURRENT APPLICATION NUMBER: US/09/102,206
PRIOR PILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 40
                                                                                                                  DB 4; Length 2040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Iida, Akihiro
APPLICANT: Hasegawa, Mamoru
APPLICANT: Hasegawa, Mamoru
APPLICANT: Hasegawa, Mamoru
APPLICANT: Nagal, Yoshiyuki
TITLE OF INVENTION: Paramyxovirus vectors used for transfer
TITLE OF INVENTION: of foreign genes
FILE REFERENCE: 50026/02501
CURRENT APPLICATION NUMBER: US/09/702,498A
CURRENT FILING DATE: 2000-10-31
                                                                                                                                                           Indels
                                                                                                              Score 17.8; DE Pred. No. 26; 0; Mismatches
; LOCATION: (B) LOCATION 1...2040
; SEQUENCE DESCRIPTION: SEQ ID NO: 2735:
US-09-107-532A-2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP 2000-152726
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
ERO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCGGCCGCAATTGAAGTTATGTAT 24
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                                                                                                                                                                                                                                                1060 GCAATCGAAGTTATTTATCCT 1080
                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09702498A Patent No. 6746860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09702498A Patent No. 674686 GENERAL INFORMATION:
APPLICANT: Tokusumi, Tsuyoshi
                                                                                                                                                                                                         7 GCAATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tokusumi, Tsuyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iida, Akihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-702-498A-4/c
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US-09-702-498A-3
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 4;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,71
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          609314 GCAGCAGCTATTGATGATATGTATCC 609339
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                                                                                                                                                                                                                                   or
g
                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: <Unknown>
                           LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c,
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TELEPHONE: (781)893-5007
                                                                                         NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                         FEATURE:
NAME/KEY: misc feature
LOCATION: (1313224)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 2735:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                            66.7%;
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.8°
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-107-532A-2735
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US-09-336-977-13/C

1 US-09-36-977-13/C

1 Sequence 13, Application US/09536977

2 Patent No. 6649409

3 GENERAL INFORMATION:
A PAPLICANT: FOMSCRAARD, ANDERS

TITLE OF INVENTION:
TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC CONSTRUCT

TITLE OF INVENTION: WATHOUT ON BASE CONSTRUCTS

FILE REFERENCE: 030307/0169

FILE REFERENCE: 030307/0169

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 06/128,558

PRIOR PELING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-03-29

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTIN OF: 2.1

SEQ ID NO 13

LENGTH: 130
                                                                                                                                                           Sequence 106, Application US/09919039
Patent No. 6727066
Patent No. 6727066
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES TITLE OF INVENTION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 106
LENGTH: 6290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 282397.85c
US-09-919-039-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.4%; Score 17.4; I
Best Local Similarity 77.8%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches
                                               4060 GCGCCAGCAGTTCAAGCTATACATCCT 4086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2117 GCGCCAGCAGTTGAAGCTATACATCCT 2091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCGCCCCCAATTGAAGTTATGTATC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (2)..(130)
US-09-536-977-13
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Weaden, Cort
TITLE OF INVENTION: Madeso, Cort
TITLE OF INVENTION: Myosin Heavy Chain (SM-MHC) Promoter/Enhancer
TITLE OF INVENTION: Myosin Heavy Chain (SM-MHC) Promoter/Enhancer
FILE REFERENCE: 00241-03
CURRENT APPLICATION NUMBER: US/09/600,319
CURRENT APPLICATION NUMBER: US/09/600,319
PRIOR APPLICATION NUMBER: PILING DATE: 1999-01-15
PRIOR APPLICATION NUMBER: 60/071,300
PRIOR PILING DATE: 1999-01-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGRAL 16011
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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPERENCE: PA.0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SEQ ID NO 224
LENGTH: 6176
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                                                                        DB 4; Length 40;
                                                                                                                      4; Indels
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; OTHER INFORMATION: Incyte ID No. 6673549 282397.77
US-09-976-594-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                      Query Match 65.2%; Score 17.6; D
Best Local Similarity 83.3%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches
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Pred. No. 50;
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                                                                                                                                                                     1 GCGGCCGCAATTGAAGTTATGTAT 24
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; Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09600319
Patent No. 6780610
; OTHER INFORMATION: Sendai virus US-09-702-498A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
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ORGANISM: Rattus norvegicus
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APPLICANT: Owens, Gary
APPLICANT: Madsen, Co
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Best Local Similarity
Matches 21; Conserva
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US-09-976-594-224
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63.0%; Score 17; DB 1; Length 131; 80.0%; Pred: No. 36; tive 0; Mismatches 5; Indels
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,294
FILING DATE: 20-SEP-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/717,294
FILING DATE: 20-SEP-1996
CLASSIFICATION NUMBER: 35
PRIOR APPLICATION NUMBER: 35
ATTORNEY/AGENT INFORMATION:
NAME: Elbing Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 36,238
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERPAX: 617-428-0200
TELERPAX: 617-428-0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
APPLICANT: HASS, JURGEN
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 GCGCCGCAGTTGAAGCTGTGCATC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCGGCCGCAATTGAAGTTATGTATC 25
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,243
FILING DATE: 19-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: LECH, KAREN F.
REGISTRATION NUMBER: 35,238
REFRENCE/DOCKET NUMBER: 00786/2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/08717294
Patent No. 6114148
                                                                                                                                                                                                                                              TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.0 Best Local Similarity 80.0 Matches 20; Conservative
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US-08-532-390-17
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STREBT: 1...
TTY: Boston
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STATE: MA
COUNTRY:
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                                                        Sequence 17, Application US/08324243
Patent No. 5786464
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: OVEREXPRESSION OF MAMMALIAN AND VIRAL
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%; Score 17; DB 1; Length 131;
80.0%; Pred. No. 36;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08532390

Patent No. 5795737

GENERAL INFORMATION:

APPLICANT: SEED, BRIAN

APPLICANT: HAAS, JURGEN

TITLE OF INVENTION: High Level Expression of Proteins

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COUNTRY: U.S.A.

ZIP: 0210-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

CURRENT APPLICATION NUMBER: US/08/532,390
                                                                                                                                                                                                                                                                                                                                                   STATE: DOBLOM
STATE: DOBLOM
STATE: DOBLOM
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,243
FILING DATE: 19-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/226001
TELECOMMUNICATION: TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S42-5070
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 20; Conservative
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US-08-324-243-17
                                                                                                                                                                                                                                                                                                         STREET: 225 F
CITY: Boston
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US-08-532-390-17/c
                                          US-08-324-243-17/c
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Gaps

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Query Match
Best Local Similarity 80.0°
Matches 20; Conservative
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US-09-536-977-43
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US-09-536-977-45/c
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Betent No. 6649409

GENERAL INFORMATION:
APPLICANT: FONSGAARD, ANDERS

TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENERIC VACCINE BASED

TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENERIC VACCINE BASED

TITLE OF INVENTION: ON A PRIMARY. BARLY HIV ISOLATE AND SYNTHETIC ENVELOPE

TITLE OF INVENTION: BX08 CONSTRUCTS

FILE REFERENCE: 030307/0169

CURRENT APPLICATION NUMBER: US/09/536,977

CURRENT PILING DATE: 2000-03-29

FRIOR APPLICATION NUMBER: 60/128,558
                                                                                            Gaps
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                                                                                                                                                                                                                                                                    CT-US95-11511-17/c
Sequence 17, Application PC/TUS9511511
Sequence 17, Application PC/TUS9511511
APPLICANT: SEED, BRIAN
TITLE OF INVENTION: OVEREXPRESSION OF MAMMALIAN AND VIRAL
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                               Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 5; Length 131;
Pred. No. 36;
                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 0.210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11511
FILING DATE:
                                        ch 63.0%; Score 17; DB 3; 1 Similarity 80.0%; Pred. No. 36; 20; Conservative 0; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.0%; Score 17; DB
80.0%; Pred. No. 36;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/226001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                              131 GCCGCCGCAGTTGAAGCTGTGCATC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 gccgccgcagrrgaagcrgrgcarc 107
                                                                                                                                    1 GCGCCCCAATTGAAGTTATGTATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCGCCCCAATTGAAGTTATGTATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.09
Matches 20; Conservative
                                        Query Match
Best Local Similarity
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PCT-US95-11511-17
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US-09-536-977-43/c
US-08-717-294-17
                                                                                       Matches
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Sequence 196, Application US/09134000C

Fatent No. 6617156

Fatent No. 6617156

FATENEAL INFORMATION:

APPLICANT: Lynn boucette-Stamm et al

TITLE OF INVENTION: EXTERNOCCIOS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EXTERNOCCIOS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: MUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

FRIOR APPLICATION NUMBER: US 60/055,778

FRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 196

EINGTH: 603
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APPLICANT: FOMSGAARD, ANDERS
TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLECTIDE SEQUENCE CONSTRUCT
TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLECTIDE SEQUENCE CONSTRUCT
TITLE OF INVENTION: METHOD FOR SEALY HIV ISOLATE AND SYNTHETIC ENVELOPE
TITLE OF INVENTION: DAY PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
TITLE OF INVENTION: DAY BOOK CONSTRUCTS
FILE REPERENCE: 030307/0169
CURRENT APPLICATION NUMBER: US/09/536,977
CURRENT FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 45
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Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: DK PA1999 00427
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 GCCGCCGCAGTTGAAGCTGTGCATC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 GCGCCCAAATTCAAGTGATTTACC 562
                                                                                                                                                                                      TYPE: DNA ORGANISM: Human immunodeficiency virus FEATURE: NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGGCCGCAATTGAAGTTATGTATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCGCCCCAATTGAAGTTATGTATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/09536977
Patent No. 6649409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Enterococcus faecalis
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80.0%;
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Sequence 35, Application US/09475515A Patent No. 6602705
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                                                                                                                                   63.0%;
80.0%;
                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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APPLICANT: BARNETT,
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LENGTH: 1323
TYPE: DNA
SEQ ID NO 49
LENGTH: 1277
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Sequence 49, Application US/09536977

Patent No. 6649409

GENERAL INFORMATION:

APPLICANT: FONSGAARD, ANDERS

TITLE OF INVENTION:

TITLE OF INVENTION:

MITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: BX08 CONSTRUCTS

TITLE OF INVENTION: BX08 CONSTRUCTS

FILE REFERENCE: 030307/0169

CURRENT APPLICATION NUMBER: 60/128,558

PRIOR APPLICATION NUMBER: 60/128,558

PRIOR APPLICATION NUMBER: DK PA1999 00427

PRIOR FILING DATE: 1999-03-29

MUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FONSGAARD, ANDERS
APPLICANT: FONSGAARD, ANDERS
TITLE OF INVENTION: MITHO PETMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
TITLE OF INVENTION: WITH OPPIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
TITLE OF INVENTION: MATHORITY BARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
TITLE OF INVENTION: BASE CONSTRUCTS
FILE REPERENCE: 030307/0169
CURRENT APPLICATION NUMBER: 05/05/97
CURRENT FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 47
LENGTH: 1277
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                                                                                                                                                                            63.0%; Score 17; DB 4; Length 1277; 80.0%; Pred. No. 58;
                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                               1041 GCCGCCGCAGTTGAAGCTGTGCATC 1017
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ORGANISM: Human immunodeficiency virus
                                           ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                   1 GCGCCGCAATTGAAGTTATGTATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCGCCCCAATTGAAGTTATGTATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/09536977
Patent No. 6649409
                                                                                                                                                       Query Match
Best Local Similarity 80.07
Best Local Similarity
20; Conservative
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Best Local Similarity 80.07
Matches 20, Conservative
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                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(1275)
US-09-536-977-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , NAME/KEY: CDS
; LOCATION: (1)..(1275)
US-09-536-977-47
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US-09-536-977-49/c
                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
US-09-536-977-47/c
LENGTH: 1277
                         TYPE: DNA
                                                                    FEATURE:
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GENERAL INFORMATION:

APPLICANT: FONGGAARD,
ANDERS

APPLICANT: FONGGAARD,
ANDERS

TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
TITLE OF INVENTION: BXOB CONSTRUCTS
TITLE OF INVENTION: BXOB CONSTRUCTS
FILE REPRERENCE: 030307/0169
CURRENT APPLICATION NUMBER: 05/09/536,977
CURRENT PILING DATE: 1099-04-09
PRIOR APPLICATION NUMBER: 06/128,558
PRIOR APPLICATION NUMBER: DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 5: 118
SEQ ID NO 5: 117
ILENGTH: 1277
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APPLICANT: HARTOG, Karin
APPLICANT: GREEK, Carherine
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICANTION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                         DB 4; Length 1277;
58;
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                                                                                                                                                               5; Indels
                                                                                                      Score 17; DB (
; Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                            1041 GCCGCCGCAGTTGAAGCTGTGCATC 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1041 GCCGCCGCAGTTGAAGCTGTGCATC 1017
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-09-536-977-49
                                                                                                                                                                                                                        1 GCGGCCGCAATTGAAGTTATGTATC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-09-536-977-51
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TYPE: DNA ORGANISM: Human immunodeficiency virus
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STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                      ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1428)
US-09-536-977-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 26
US-08-324-243-34/c
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US-09-475-515-33/c
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SEQ ID NO 73
LENGTH: 14
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Sequence 73, Application US/09536977

Batent No. 6649409

GENERAL INFORMATION:

APPLICANT: FORSGAARD, ANDERS

TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: MATH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: MATH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: MATH OFTIMIZED

TITLE OF INVENTION: MADER: US/09/536,977

CURRENT FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR PELING DATE: 1999-03-29

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTIN VET: 2.1
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APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIU, HARTOG, Karin
APPLICANT: SLEER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: INFOVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: L621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver: 2.0
SED ID NO 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                           Query Match 63.0%; Score 17; DB 4; Length 1323; Best Local Similarity 80.0%; Pred. No. 58; Matches 20; Conservative 0; Mismatches 5; Indels
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                                                  OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: gp120.modSF162.delV1V2
US-09-475-515-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: gp120.modSF162.delV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1044 GCCGCCGCAGTTGAAGCTGTGCATC 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 34, Application US/09475515A; Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Seguence
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US-09-475-515-34/c
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US-09-536-977-73/c
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APPLICANT: LIU, Hong
APPLICANT: GEER, Catherine
APPLICANT: SELEY, Mark
APPLICANT: SELEY, Mark
APPLICANT: SELEY, Mark
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT PILING DATE: 1999-12-30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
LENGTH: 1453
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Score 17; DB 4; Length 1431;
Pred. No. 59;
0; Mismatches 5; Indels
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Patent No. 5786464
GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
TITLE OF INVENTION: OVEREXPRESSION OF MAMMALIAN AND VIRAL
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                      1041 gcceccecacricaaecrerecare 1017
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                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/09475515A Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, INDRESH
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
             63.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
           Query Match 63.0
Best Local Similarity 80.0
Matches 20, Conservative
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Gaps
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                                                 63.0%; Score 17; DB 1; Length 1632;
80.0%; Pred. No. 61;
ive 0; Mismatches 5; Indels
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Pred. No. 61;
0; Mismatches 5; Indels
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TITLE OF INVENTION: OVEREXPRESSION OF MANMALIAN AND VIRAL
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,294
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY'---
ATTORNEY'---
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HAAS, JURGEN
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
CORRESPONDENCE: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                1230 GCCGCCGCAGTTGAAGCTGTGCATC 1206
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                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/08717294
Patent No. 6114148
GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
APPLICANT: HAAS, UNGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.0%;
Best Local Similarity 80.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ for Wir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,2
                                                      Query Match 63.0
Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Bos
STATE: MA
COUNTRY:
     US-08-532-390-34
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Patent No. 5795737
GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JURGEN
TITLE OF INVENTION: High Level Expression of Proteins
NUMBER OF SEQUENCES: 40
CORRESPONDENCES: 40
CORRESPONDENCES: AbDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIREE: 1. 425 Franklin Street
CITY: Massachusetts
COUNTRY: U.S.A.
ZIP: 0.210-2804
ZIP: 0.2110-2804
COMPUTER READABLE FORM:
MEDIUM TYPES: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,390
FILING DATE: 22-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/24,243
ATTONEY/AGENT INPORMATION:
REGISTRATION NUMBER: 35,238
                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
IS ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL.
REGISTRANTAL NUMBER: 00.086/226001
TELECOMMUNICATION NUMBER: 00.086/226001
TELECOMMUNICATION IS A2-5070
TELEPRAX: (6.17) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1230 decedecederica de crerecare 1206
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1 TOPOLOGY: linear
US-08-324-243-34
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER:STICS:
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US-08-532-390-34/c
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APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIV, HONG
APPLICANT: LIV, HONG
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002.
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 4 stentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HARNOG, Karin
APPLICANT: HARNOG, Karin
APPLICANT: HARNOG, Karin
APPLICANT: GREEK, Catherine
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VRUSS-LIKE PARTICLES
FILE REFERENCE: 1621.002
TITLE OF SEPTION NUMBER: US/09/475,515A
CURRENT PALLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN VET. 2.0
SEG ID NO 47
LENGTH: 1836
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  Gaps
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5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: gp140.mut7.modSF162.delV1/V2
US-09-475-515-44
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OTHER INFORMATION: Description of Artificial Sequence:
  0; Mismatches
                                                                                         936 écceccecagireaacrerecare 912
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                                           1 GCGGCCGCAATTGAAGTTATGTATC
                                                                                                                                                                                                         Sequence 44, Application US/09475515A Patent No. 6602705
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Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: ZUR REGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
  20; Conservative
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    Matches
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APPLICANT: LIAN, Ying
APPLICANT: LIU, Hong
APPLICANT: Gatherine
APPLICANT: GELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
FITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: gp140.mut.modSF162.delV1/V2
US-09-475-515-41
                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%; Score 17; DB
80.0%; Pred. No. 61;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/226001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1230 GcccccccccrrcaAccrcrccarc 1206
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                                                                                              CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/09475515A Patent No. 6602705 GENERAL INFORMATION:
                                                     Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELBEAX: (61.,
TELEFAX: 0.0154
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0°
       TUMBER OF SEQUENCES: 37
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PCT-US95-11511-34
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Best Local Similarity
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US-09-475-515-41/c
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US-09-475-515-38/c
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GENERAL INCOMATION:

GENERAL INCOMATION:

APPLICANT: FORMSTAND.

TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLECTIDE SEQUENCE CONSTRUCT

TITLE OF INVENTION: WITH OFTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED

TITLE OF INVENTION: WAS CONSTRUCTS

TITLE OF INVENTION: BXO8 CONSTRUCTS

FILE REFERENCE: 030307/0169

CURRENT APPLICATION NUMBER: 060128,558

PRIOR APPLICATION NUMBER: D60128,558

PRIOR PILING DATE: 1999-04-09

PRIOR PILING DATE: 1999-03-29

NUMBER OF SEQ ID NOS: 118

SOSTWARE: PALENTIN VEY: 2.1
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: RIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: HANG, Karin
APPLICANT: GERER, Catherine
APPLICANT: GERER, Catherine
APPLICANT: WALKER, Christopher
APPLICANT: WELKER, Christopher
TITLE OF INVENTION: DF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT PEPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 37
TYPE: DNA
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                                                             Length 1836;
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                                                                                                          5; Indels
; OTHER INFORMATION: gp140.mut8.modSF162.delV1/V2
US-09-475-515-47
                                                             Score 17; DB 4;
Pred. No. 63;
0; Mismatches
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80.0%; Pred. No. 6
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                                                                                                                                                                                            936 GCCGCCGCAGTTGAAGCTGTGCATC 912
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                                                                                                                                                                                                                                                                                                       Sequence 67, Application US/09536977
Patent No. 6649409
                                                           / Match 63.0%;
Local Similarity 80.0%;
hes 20; Conservative
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Best Local Similarity 80.0
Matches 20; Conservative
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APPLICANT: BARNETT, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: CDS
; LOCATION: (1)..(1905)
US-09-536-977-67
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US-09-536-977-67/c
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LENGTH: 1918
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                                                               Query Match
                                                                                                          Matches
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APPLICANT: LIAN, Ying
APPLICANT: LIU, Hong
APPLICANT: LIU, Hong
APPLICANT: SELBY, Mark
TITLE OF INVENTION: INFROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
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Pred. No. 63;
                                                                                                                                                                      Indels
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) ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: gpl40.modSF162.delV2
US-09-475-515-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: gp140.modSF162.delV1/V2
US-09-475-515-38
                                                                                                                          Score 17; DB 4
Pred. No. 63;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Application US/09475515A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
                                                                                                                                                                                                                                                                                                                                                                                                                        BARNETT, Susan
ZUR MEGEDE, Jan
SRIVASTAVA, Indresh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPB: DNA
ORGANISM: Artificial Sequence
                                                                                                                        y match 63.0%;
Local Similarity 80.0%;
hes 20; Conservative (
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SEQ ID NO 38
LENGTH: 1944
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TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION ITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.0%; Score 17; DB 4; Length 1944; Best Local Similarity 80.0%; Pred. No. 63; Matches 20; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: gp140.mut8.modSF162.delV2
                                            FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER FEG IN NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1044 GCCGCCGCAGTTGAAGCTGTGCATC 1020
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APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BARNETT, Susan
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US-09-475-515-39/c
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                                                                                                                                                                                                                                                             FEATURE:
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APPLICANT: GEER, Catherine
APPLICANT: GEER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Chistopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REPERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 63;
0; Mismatches 5; Indels
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Pred. No. 63;
0; Mismatches 5; Indels
                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: gp140.mut.modSF162.delV2
US-09-475-515-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43, Application US/09475515A
Patent No. 6602705
GENERAL INFORMATION:
APPLICANT: EARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SILVASTRA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/09475515A Patent No. 6602705
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: LIU, Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%;
80.0%;
                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0%;
Matches 20; Conservative
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ORGANISM: Artificial Sequence
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SELBY, Mark
WALKER, Christopher
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
LENGTH: 1944
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Best Local Similarity 80.0%
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US-09-475-515-43/c
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LENGTH: 1944
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                                                                                                                                         FEATURE:
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APPLICANT: SRIVASTAVA, Indresh
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIN, Ying
APPLICANT: LIN, Ying
APPLICANT: LIU, Hong
APPLICANT: LIU, Hong
APPLICANT: BLBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
ITITE OF INVENTION: INPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
ITITE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 2025
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Gaps
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APPLICANT: LIU, Hong
APPLICANT: GREER, Catherine
APPLICANT: GREER, Catherine
APPLICANT: GREER, Catherine
APPLICANT: GREER, Catherine
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
CURRENT FILING DATE: 1999-12-30
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: DATA
CORGANISM: Artificial Sequence
FRANUE:
OTHER INFORMATION: GP140.mut.modSF162
OTHER INFORMATION: GP140.mut.modSF162
US-09-475-515-39
Query Match
Best Local Similarity 80.0%; Pred. No. 64;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Search completed: January 7, 2005, 11:00:35 Job time : 53.7895 secs

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4121
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2541
16011
                    64.4
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-940-544-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
  Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 98, Appl
Sequence 1316, Ap
Sequence 1316, Ap
Sequence 1, Appli
Sequence 257, App
Sequence 257, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 256, Appli
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                                                                                                                                                          (without alignments)
134.979 Million cell updates/sec
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                                                                                                                                       January 7, 2005, 11:00:44; Search time 1147.74 Seconds
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1: \cgn2 \( \) \cgn\( \) \c
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 US-09-997-722-258

US-09-738-546-1

US-09-836-544-7

5 US-10-207-655-98

6 US-10-641-643-1316

5 US-10-641-643-1316

5 US-10-641-643-1316

5 US-10-143-238-1

1 US-09-93-297-3

1 US-09-93-256
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                                                                                                                                                                                                                                                                                                                                                         4293498 segs, 2868903791 residues
                                                                                                                                                                                                                 US-09-786-502A-7
27
1 gcggccgcaattgaagttatgtatcct 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                           Searched:
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3804 3806 51365

1514 3803

20110

Result

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Sequence 1, Application US/08940544B

| Sequence 1, Application No. US20020018783A1
| CHENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: SADELAIN, MICHEL
| APPLICANT: CHEUNG, NAI-KONG V.
| TITLE OF INVENTION: FUESTON FROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND TITLE OF INVENTION: USES THEREOF
| TITLE OF INVENTION: USES THEREOF
| FILE REFERENCE: MSK. P-035-US
| CURRENT APPLICATION NUMBER: US/08/940,544B
| CURRENT FILING DATE: 1997-09-30
| KARINER APPLICATION NUMBER: PCT/US97/04427
| EARLIER FILING DATE: 1997-03-20
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PATENTIN Ver. 2.0
| SEQ ID NO 1
| LENGTH: 27
                                              Sequence 2623, Ap Sequence 2623, Ap Sequence 21, Appl Sequence 19, Appl Sequence 25, Appl Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 33246, Appl Sequence 33246, Appl Sequence 16, Appl Sequence 5599, Appl 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1095, Ap
Sequence 1095, Ap
Sequence 1391, Ap
Sequence 15342, A
Sequence 264609,
Sequence 264609,
Sequence 264609,
Sequence 264609,
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       Sequence 11,
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100.0%; Score 27; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 27; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Upstream primer for PCR amplification
US-10-027-632-264609
US-10-027-632-264609
US-10-425-115-68262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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CURRENT APPLICATION NUMBER: US/09/738,546
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/170,857.
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
LENGTH: 1514
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Patent No. US2002006403A1
GENERAL INFORMATION:
APPLICANT: YU, XUB-ZHONG
APPLICANT: ANASETI, CLAUDIO
TITLE OF INVENTION: CD28-SPECIFIC ANTIBODY COMPOSITIONS FOR USE IN METHODS
TITLE OF INVENTION: OF INMUNOSUPPRESSION
FILE REPERENCE: FHCC:007US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mortis, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FITLE OF INVENTION: NUMBER: US/09/997,722
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT APPLICATION NUMBER: US/09/997,722
FRIOR APPLICATION NUMBER: US/09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFFWARE: Patentin version 3.1
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Pred. No. 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                 Sequence 6, Application US/10448256

Publication No US20040043401A1

GERRAL INFORMATION:
APPLICANT: Sadelain, Michel
APPLICANT: Brentjens, Renier
APPLICANT: Maher, John
TITLE OF INVENTION: Chimeric T Cell Receptors
FILE REFERENCE: MSK.P-058
CURRENT FILING DATE: 2003-05-28
FRIOR FILING DATE: 2003-05-28
FRIOR FILING DATE: 2002-05-28
FRIOR FILING DATE: 2002-05-38
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
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; Sequence 258, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
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100.0%; Pre
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Best Local Similarity 100.
Matches 19; Conservative
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CORGANISM: Homo sapiens
US-09-997-722-258
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: human
US-10-448-256-6
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LENGTH: 663
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US-09-738-546-1
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APPLICANT: Hayden-Ledbetter, Martha S.
FILLE HAYDEN-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
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                                                                                                                                                                        Length 1514;
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APPLICANT: The General Hospital Corporation

TITLE OF INVENTOR: Rapid Immunoselection Cloning Method

FILE OF INVENTOR: Rapid Immunoselection Cloning Method

FILE REFERENCE: 11-86L

CURRENT APPLICATION NUMBER: US/09/836,544

CURRENT FILING DATE: 2001-04-17

PRIOR APPLICATION NUMBER: US 07/533,759

PRIOR FILING DATE: 1990-07-13

PRIOR FILING DATE: 1990-07-13

PRIOR PLING DATE: 1990-07-13

PRIOR PLING DATE: 1990-07-13

PRIOR PLING DATE: 1989-07-13

PRIOR PLING DATE: 1989-07-13

PRIOR FILING DATE: 1989-07-13

PRIOR PRIOR PRIOR DATE: 1989-07-13

PRIOR PRIOR PRIOR DATE: 1989-07-13

PRIOR FILING DATE: 1989-07-13
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Publication No. US20030118592A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09836544 Publication No. US20040072283A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            438 AATTGAAGTTATGTATCCT 456
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Best Local Similarity 100.0
Matches 19; Conservative
TYPE: DNA
ORGANISM: Homo sapiens
US-09-738-546-1
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LOCATION: (100)..(759)
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US-10-207-655-98
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US-10-076-934-1
; Sequence 1, Application US/10076934
; Publication No. US20030170232A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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ORGANISM: Homo sapiens
US-09-997-722-257
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA; ORGANISM: Homo sapiens
US-10-076-934-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-997-722-257
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US-10-143-238-1
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                                                                                                                                                                                             Gaps
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Sugan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
                                                                                                                                                                                             ö
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                                                                                                                                                Query Match 70.4%; Score 19; DB 15; Length 1514; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PEFFECT 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 1316 : US-10-641-643-1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-10-641-643-1316
; Sequence 1316, Application US/10641643
; Publication No. US20040077003A1
; GENEAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                                                                                               438 AATTGAAGTTATGTATCCT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1514 base pairs
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                                                                                                                                                                                                                                       9 AATTGAAGTTATGTATCCT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (650) 845-416
INFORMATION FOR SEQ ID NO: 1316:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
SOFTWARE: Patentin version 3.0 SEQ ID NO 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOPOLOGY: linear
                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-98
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Sequence 1, Application US/10143238
Publication No. US20030166502A1
GENERAL INFORMATION:
APPLICANT: Green, Jonathan M.
APPLICANT: Shaw, Andrey S.
TITLE OF INVENTION: DIFFERENTIAL REGULATION OF T CELL SURVIVAL AND TITLE OF INVENTION: DIFFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 257, Application US/0999722

Sequence 257, Application US/0999722

Publication No. US20040072154A1

GENERAL INFORMATION:
APPLICANT: Morris, David

APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REPERENCE: A-71171/RMS/DCF

CURRENT APPLICATION NUMBER: US 09/797,722

CURRENT PILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: US 09/794,586

PRIOR PILING DATE: 2001-12-22

PRIOR PILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 301

SEQ ID NO 257

LENGTH: 3804
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APPLICANT: O'Hara Jr., Richard
APPLICANT: O'Hara Jr., Richard
APPLICANT: Nagelin, Ann Marie
TITLE OF INVENTION: AGENTS THAT SPECIFICALLY BLOCK
TITLE OF INVENTION: CD28-MEDIATED SIGNALING AND USES THEREFOR
FILE REFERENCE: GNN-028
CURRENT APPLICATION NUMBER: US/10/076,934
CURRENT FILING DATE: 2002-02-19
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3803;
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.4%; Score 19; DB 15; I 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3803
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NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version
SEQ ID NO 256
LENGTH: 51365
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| Publication No. US20030086932A1
| GENERAL INFORMATION:
| APPLICANT: Bluestone, Jeffrey
| APPLICANT: Collins, Mary
| APPLICANT: Califin, Mathew
| APPLICANT: Califin, Mathew
| APPLICANT: Kranz, David
| TITLE OF INVENTION: THAT BIND TO CTLA4 AND USES THEREFOR
| TITLE OF INVENTION: THAT BIND TO CTLA4 AND USES THEREFOR
| FILE REPERENCE: GNN-014CP
| CURRENT FALICATION NUMBER: US/09/835,297
| PRIOR APPLICATION NUMBER: 2001-04-12
| PRIOR APPLICATION NUMBER: 2000-04-12
| PRIOR FILING DATE: 2000-04-12
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 3
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US-09-997-722-256

Sequence 256, Application US/09997722

Sequence 256, Application US/09997722

Publication No. US20040072154A1

GENERAL INFORMATION:

APPLICANT: MORTIG, David

APPLICANT: APPLICATION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REPERBNCE A-71171/RNS/DCF

CURRENT APPLICATION NUMBER: US/09/997,722

CURRENT FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-103-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3806;
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0;
; FILE REFERENCE: GNN-030
; CURRENT APPLICATION NUMBER: US/10/143,238
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/290,097
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEO ID NO 1: SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (223)...(885)
US-10-143-238-1
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-835-297-3
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US-10-097-111-10

Sequence 10, Application US/10097111

Bequence 10, Application US/10097111

CENERAL INFORMATION:
APPLICANT: PELLETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: GROS, PHILLIPPE
APPLICANT: GROS, PHILLIPPE
APPLICANT: ON S. SEQUENCES FROM S. PNEUMONIAE BACTERIOPHAGE EPI THAT
TITLE OF INVENITON: ENCODE ANTI-MICROBIAL POLYPEPTIDES
FILE REFERENCE: 073406-0603
CURRENT APPLICATION NUMBER: US/10/097,111

CURRENT APPLICATION NUMBER: 09/676,412
PRIOR PILING DATE: 2000-09-29
PRIOR FILING DATE: 1999-99-30
NUMBER OF SEQ ID NOS: 552
SEQ ID NO 10
LENGTH: 56506
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-097-111-11
i Gequence 11. Application US/10097111
i Beduence 11. Application US/10097111
i Publication No. US20030138771A1
i GENERAL INFORMATION:
i APPLICANT: BLIETIER, JERRY
i APPLICANT: DUBOW, MICHAEL
i TITLE OF INVENTION: DNA SEQUENCES FROM S. PNEUMONIAE BACTERIOPHAGE EP1 THAT
TITLE OF INVENTION: BNCODE ANTI-MICROBIAL POLYPEPTIDES
i TITLE OF INVENTION: 2002-07-24
i FILE REFERENCE: 073406-0603
i CURRENT FILING DATE: 2002-07-24
i PRIOR FILING DATE: 2000-09-29
i PRIOR FILING DATE: 1999-09-30
i NUMBER OF SEQ ID NOS: 552
i SOFTWARE: Patentin Ver. 2.1
i SEQ ID NO 11
i LENGTH: 3693
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                                                                                                                                                                              Length 51365;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                           Query Match 70.4%; Score 19; DB 11; I
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1582 GCCGCAACTGAAGTCATGTATGC 1604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                9 AATTGAAGTTATGTATCCT 27
PatentIn version 3.1
                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-722-256
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLLING DATE: 2000-03-21
PRIOR PLLING DATE: 2000-03-23
PRIOR PLLING DATE: 2000-05-23
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-06
PRIOR PLLING DATE: 2000-05-06
PRIOR PLLING DATE: 2000-05-09
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLLING DATE: 2001-02-09
PRIOR PLLING DATE: 2001-02-09
PRIOR PLLING DATE: 2001-02-06
PRIOR PLLING DATE: 2001-02-16
PRIOR PLLING DATE: 2010-02-16
PRIOR PLING DATE: 2010-02-17
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80.8%; Pred. No. 3.6e+02;
ive 0; Mismatches 5; Indels
PRIOR FILING DATE: 2001-02 C
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 2623
LENGTH: 2000
TYPE: DNA
ORGANISM: Oryza Sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1484 GCAGCCGCATTCGAAGGTGTGTATCC 1509
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: N region
LOCATION: (1674)
COTHER INFORMATION: n = any nucleotide
US-10-260-238-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.84
Matches 21; Conservative
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Wall, Daniel
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APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                      Query Match 67.4%; Score 18.2; DB 15; Length 56506; Best Local Similarity 87.0%; Pred. No. 4.9e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0;
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TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REPERENCE: 60111-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.7%; Score 18; DB 17; Length 1112; Best Local Similarity 80.8%; Pred. No. 3.3e+02; Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_94799C.1
US-10-437-963-96729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(1112)
OTHER INFORMATION: unsure at all n locations
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; Sequence 96729, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCGCCCCAATTGAAGTTATGTATCC 26
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PRIOR APPLICATION NUMBER: US 60/325,448
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US-10-260-238-2623
; Sequence 2623, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
   ; ORGANISM: Streptococcus pneumoniae US-10-097-111-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Provart, Nicholas
Ricke, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 96729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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Sequence 16, Application US/10697828
; Dedication No. US20040185546A1
; Cardence 16, Application US/10697828
; Publication No. US20040185546A1
; GENERAL INFORMATION:
    APPLICANT: Rosen, Jin Kyu
    APPLICANT: Lee, Jin Kyu
    APPLICANT: Hemmerich, Stefan
    TITLE OF INVENTION: NOVel Glycosyl Sulfotransferases GST-4alpha, GST-4beta, & GST-6
    FILE REFERENCE: UCAL-138DIV
    CURRENT PILING DATE: 2003-10-29
    PRIOR APPLICATION NUMBER: 09/593,828
    PRIOR PILING DATE: 2000-06-13
    PRIOR PILING DATE: 1999-07-20
    NUMBER OF SEQ ID NOS: 23
    SOFTWARE: PastSEQ for Windows Version 4.0
    SEQ ID NO 16
    LENGTH: 5084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 48445;
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Sequence 25, Application US/10087192

Sequence 25, Application US/10087192

BUBLICALION NO. US20020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David W.

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

FILE REFERENCE: 52245200122

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2069

SOFTWARE FRANCES FOR WINGOWS VERSION 4.0

SEQ ID NO 25

LENGTH: 48445
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2788 GCAAGTGAAGTTTTGTATCCT 2768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3288 GCAAGTGAAGTTTTGTATCCT 3268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 GCAATTGAAGTTATGTATCCT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (1)...(48445)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: mouse US-10-697-828-16
                                                                                                                                US-10-697-828-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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Sequence 19, Application US/10697828

Sequence 19, Application US/10697828

Publication No. US20040185546A1

GENERAL INFORMATION:
APPLICANT: Rosen, Steven
APPLICANT: Hemmerich, Stefan
TILE OF INVENTION: Novel Glycosyl Sulfotransferases GST-4alpha, GST-4beta, & GST-6

TILE REFERENCE: UCAL-138DIV
CURRENT APPLICATION NUMBER: US/10/697,828

CURRENT FILING DATE: 2003-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PLING DATE: 1090-00-613
PRIOR PLING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 19

SEQ ID NO 19

LENGTH: 4121
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen, Steven
APPLICANT: Rosen, Steven
APPLICANT: Lee, Jin Kyu
APPLICANT: Hemerich, Stefan
TITLE OF INVENTION: NOVel Glycosyl Sulfotransferases GST-4alpha, GST-4beta, & GST-6
FILE REFERENCE: UCAL-138DIV
CURRENT APPLICATION NUMBER: US/10/697,828
CURRENT FILING DATE: 2003-310-29
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 1999-07-20
NUMBER: OF SEQ ID NOS: 23
SDFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 3624
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                                                     Query Match 65.9%; Score 17.8; DB 16; Length 2178; Best Local Similarity 90.5%; Pred. No. 4.5e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                          1042 GCAATCGAAGTTATTTATCCT 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2788 GCAAGTGAAGTTTTGTATCCT 2768
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's Sequence 23, Application US/10697828

'Publication No. US20040185546Al

GENERAL INFORMATION:
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Best Local Similarity 90.5
Matches 19; Conservative
     JS-10-282-122A-21821
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; ORGANISM: mouse
US-10-697-828-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: mouse
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                                                                                                                                                                                                                                                                          Query Match 65.2%; Score 17.6; DB 9; Length 40; Best Local Similarity 83.3%; Pred. No. 2.9e+02; Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-277-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Artificially Synthesized Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP FILE REFERENCE: 50026/029001
CURRENT APPLICATION NUMBER: US/09/966,930
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/JP00/03194
PRIOR APPLICATION NUMBER: DT 2001/283451
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 1001-09-18
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 21
LENGTH: 40
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 64
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                              1 GCGCCCCAATTGAAGTTATGTAT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCGGCCGCAATTGAAGTTATGTAT 24
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US-09-966-930-22/C
US-09-966-930
Sequence 22, Application US/09966930
Publication No. US20030022376A1
GENERAL INFORMATION:
APPLICANT: KITAZATO, Kaio
APPLICANT: SHU, Tsugumine
                                                                                                                                                                                                                                                                                                                                                                                                                           26 GCGCCCCAATGCCAGATATCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09966930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ASAKAWA, MAKOTO
APPLICANT: HASEGAWA, Mamoru
APPLICANT: IIDA, ARIHITO
APPLICANT: HIRATA, TAKAHITO
APPLICANT: INOUE, MAKOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHU, Tsugumine
KUMA, Hidekazu
UEDA, Yasuji
ASAKAWA, Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KITAZATO, Kaio
APPLICANT: SHU, Tsugumine
APPLICANT: KUMA, Hidekazu
APPLICANT: UEDA, Yasuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 20; Conserv
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APPLICANT:
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                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHU, TSUGUMINE
APPLICANT: WITAZAZO, Kaio
APPLICANT: WEMA, Hidekazu
APPLICANT: WEMA, Hidekazu
APPLICANT: WEDA, Yasuji
APPLICANT: HASEGAWA, Mamoru
APPLICANT: HASEGAWA, Mamoru
APPLICANT: TOKITOU, Fumino
APPLICANT: TOKITOU, Fumino
APPLICANT: TOKITOU, Fumino
APPLICANT: TOKITOU, Fumino
APPLICANT: TOKITOU: WEMOIN: APPLICANT:
INOUE, MAKOTO
ITILE OF INVENTION: WECONE
FILE REFERENCE: 50026/028001
CURRENT FILING DATE: 2001-09-27
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PRASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TOKITOU, Funino
APPLICANT: TOKITOU, Funino
APPLICANT: HIRATA, Takahiro
APPLICANT: TOKUSUMI, Teuyoshi
APPLICANT: TOKUSUMI, Teuyoshi
APPLICANT: INOUE, Makoto
1TITLE OF INVENTION: WECTOR
1TITLE OF INVENTION: VECTOR
1TITLE OF INVENTION: VECTOR
1TITLE OF INVENTION: VECTOR
1CURRENT APPLICATION NUMBER: US/09/966,277
CURRENT PELING DATE: 2001-09-27
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: JP 101/200739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.2%; Score 17.6; DB 9; Length 4 Best Local Similarity 83.3%; Pred. No. 2.9e+02; Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-277-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCGCCCCAATTGAAGTTATGTAT 24
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                                                                                  Sequence 21, Application US/09966277
Patent No. US20020169306Al
GENERAL INFORMATION:
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Patent No. US20020169306A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASAKAWA, Makoto
HASEGAWA, Mamoru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KITAZATO, Kaio
APPLICANT: SHU, Tsugumine
APPLICANT: KUMA, Hidekazu
APPLICANT: UEDA, Yasuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIDA, Akihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 23
US-09-966-277-22/c
                                        RESULT 22
US-09-966-277-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 21
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
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Length 40; Indels

Score 17.6; DB 15; Pred. No. 2.9e+02; 0; Mismatches 4;

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Query Match 65.2%;
Best Local Similarity 83.3%;
Matches 20; Conservative
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-316-538-22
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OTHER INFORMATION: Description of Artificial Sequence: artificially
1. OTHER INFORMATION: synthesized sequence
US-10-316-538-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Artificially Synthesized Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.6; DB 10;
Pred. No. 2.9e+02;
0; Mismatches 4;
                                APPLICANT: HIRATA, TAKABLICO
APPLICANT: HIRATA, TAKABLICO
TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP
FILE BEFERENE: 500.26/02.001
CURRENT APPLICATION NUMBER: US/09/966,930
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/JP00/03194
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-18
PRIOR FILING DATE: 1999-05-18
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 2:
LENGTH: 40
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APPLICANT: HOUGE, MARCEO
APPLICANT: TOWUE, MARCEO
TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP
FILE REPERBURG: D3-102PCT-USCI
CURRENY APPLICATION NUMBER: US/10/316,538
CURRENY FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/JP02/09558
PRIOR APPLICATION NUMBER: US 09/966,930
PRIOR FILING DATE: 2001-09-27
PRIOR PELICATION NUMBER: UP 2001-283451
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 1999-05-18
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 20; Conservative
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ORGANISM: Artificial Sequence
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IIDA, Akihiro
HASEGAWA, Mamoru
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
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APPLICANT: SHU, Tsugumine
APPLICANT: KUMA, Hidekazu
APPLICANT: UEDA, Yasuji
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US-10-316-538-21
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TOKUSUMI, Yumiko
TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP
FILE REFERENCE: D3-102PCT-USC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE D3-102FC1-02C1
CURRENT APPLICATION NUMBER: US/10/316,538
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US/10/0258
PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 09/966,930
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 22
LENGTH: 40
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                                                                                                                                     Sequence 22, Application US/10316538
Publication No. US20030166252A1
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Publication No. US20030170266A1
GENERAL INFORMATION:
APPLICANT: KITAZATO, Kaio
APPLICANT: SHU, TSUGumine
APPLICANT: SHU, Hidekazu
APPLICANT: UEDA, Yasuji
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IIDA, Akihiro
HIRATA, Takahiro
INOUE, Makoto
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TOKITOU, Fumino
HIRATA, Takahiro
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TOKUSUMI, Tsuyosh
                                                                                                                                                                                                              APPLICANT: KITAZATO, Kaio
APPLICANT: SHU, Tsugumine
APPLICANT: KUMA, Hidekazu
APPLICANT: UEDA, Yasuji
APPLICANT: ASAKAMA, MAKOCC
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US-10-784-710-4/C
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LENGTH: 40
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APPLICANT: INVOL, MANCLO
APPLICANT: TOKUCH, MANCLO
TITLE OF INVENTION: ENVELORE GENE-DEFICIENT PARAMYXOVIRUS VECTOR
FILE REPREBICE: D3-103PCT-USC1
CURRENT APPLICATION NUMBER: US/10/316,535
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/JP02/0958
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
SOFTWARE: PEATON NUMBER: D7 1999-200739
PRIOR FILING DATE: 2000-05-18
SOFTWARE: PATENTING DATE: 2000-05-18
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TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS VECTOR
FILE REPRENEUR: D3-103PCT-USC1
CURRENT APPLICATION NUMBER: US/10/316,535
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/JP02/09558
PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-09-17
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2001-09-18
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 1999-05-18
PRIOR PILING DATE: 1999-05-18
PRIOR PILING DATE: 1999-05-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.2%;
Best Local Similarity 83.3%;
Matches 20; Conservative
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INOUE, Makoto
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IIDA, Akihiro
TOKITOU, Fumino
HIRATA, Takahiro
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KUMA, Hidekazu
UEDA, Yasuji
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US-10-316-535-22/c
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificially; OTHER INFORMATION: synthesized sequence
US-10-316-535-22
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GENERAL INFORMATION:

APPLICANT: Idda, Akihiro

APPLICANT: Idda, Akihiro

APPLICANT: Hagai, Yoshiyuki

TITLE OF INVENTION: Paramyxovirus vectors used for transfer:

TITLE OF INVENTION: of foreign genes

TITLE OF INVENTION: of foreign genes

FILE REFERENCE: 50056/025001

CURRENT APPLICATION NUMBER: US/10/784,710

CURRENT PILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: US/09/702,498A

PRIOR PILING DATE: 2000-10-31

PRIOR PILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: INDEASONAL AND ADDRESS APPLICANT: INDEASONAL APPLICANT: Hasegawa, Mamoru APPLICANT: Hasegawa, Mamoru APPLICANT: Hasegawa, Mamoru APPLICANT: Nagai, Yoshiyuki TITLE OF INVENTION: Paramyxovirus vectors used for transfer TITLE OF INVENTION: Of foreign genes FILE REFERENCE: 50026/025001
CURRENT FILING DATE: 2004-02-23
PRIOR APPLICATION NUMBER: US/09/702,498A
PRIOR PILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                             Length 40;
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Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                   1 GCGCCCCCAATTGAAGTTATGTAT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
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Matches 20; Conserv
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Sequence 16, Application US/10057726
Publication No. US20030017549A1
GENERAL INFORMATION:
APPLICANT: Owens, Gark K.
APPLICANT: Manabe, Ichiro
TITLE OF INVENTION: SPECIFICALLY IN SMOOTH MUSCLE CELLS IN VIVO
FILE REFERENCE: 021588-000200US
CURRENT APPLICATION NUMBER: US/10/057,726
CURRENT FILING DATE: 2002-06-24
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Pred. No. 7.7e+02;
0; Mismatches 4;
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PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2000-07-13
PRIOR FILING DATE: 1000-07-13
PRIOR FILING DATE: 1999-01-15
PRIOR PILING DATE: 1999-01-15
PRIOR FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 16011
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US-09-769-736-186
iS-09-769-736-186
sequence 186, Application US/09769736
spublication No. US20030138775A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVERTION: Proteins
CURRENT APPLICATION: Proteins
FILE REFERENCE: PWC/P21089wo
CURRENT APPLICATION WUMBER: US/09/769,736
CURRENT APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 212
SOFTWARE PATENT US ALENTH VET: 2.1
SOFTWARE PATENT VET: 2.1
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Best Local Similarity 83.3
Matches 20; Conservative
; SEQ ID NO 404
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-057-726-16/c
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Excounting the control of the control of
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                   ) OTHER INFORMATION: Artificially synthesized sequence derived from the COTHER INFORMATION: Sendai virus US-10-784-710-4
                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                  Length 40;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
FILOR APPLICATION NUMBER: US/2010-04
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR PILING DATE: 2001-06-07
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4350
SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                       Query Match 65.2%; Score 17.6; DB 17; Best Local Similarity 83.3%; Pred. No. 2.9e+02; Matches 20; Conservative 0; Mismatches 4;
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US-10-437-963-33246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(2006)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33246, Application US/10437963; Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 GCGGCCGCAATGGCAGATATCTAT 3
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                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 20, Conservative
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US-10-264-049-404
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                                                                                                          FEATURE:
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ORGANISM: Zea mays
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ORGANISM: Human
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cheikh, Nordine

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Miller, Phillip W.

APPLICANT: O'COnnell, Keith M.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules

TITLE OF INVENTION: NUMBER: US/09/987,899

CURRENT FILING DATE: 2001-11-16

PRIOR FILING DATE: 1999-03-04

PRIOR FILING DATE: 1999-03-06

NUMBER OF SEQ ID NOS: 7341

SEQ ID NO 5558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Miller, Phillip W.
TITLE OF COMPELI, Keith M.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: With the Carbon Assimilation Pathway
FILE REPERBURE: 16517.258
CURRENT APPLICATION NUMBER: US/09/987,899
CURRENT FILING DATE: 2001-11-16
PRIOR PPLING DATE: 1999-03-04
PRIOR PILING DATE: 1999-03-06
PRIOR PILING DATE: 1998-03-06
MUMBER OF SEQ ID NOS: 7341

SEQ ID NO 5599
LENGTH: 154
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                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-769-736-186
                                                                                                                                                                      Length
                                                                                                                                                                                                                          Indels
                                                                                                                                                             Query Match 64.4%; Score 17.4; DB 10;
Best Local Similarity 77.8%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 6;
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US-09-987-899-5599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5599, Application US/09987899

Publication No. US20040116682A1

GENERAL INFORMATION:

APPLICANT: Cheikh, Nordine
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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US-09-987-899-5599
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US-1U-424-23-35A-1U-95/C
Sequence 1095, Application US/10242535A
Publication No. US2004001363A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITIE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
TITIE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/305,783
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin Version 3.2
LENGTH: 292
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Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT Chondrodene Inc.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT PPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28

PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: Patentin version 3.2

SEQ ID NO 1095
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                                                                                      Length 285;
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                                                                                Query Match 64.4%; Score 17.4; DB 11; Best Local Similarity 77.8%; Pred. No. 5e+02; Matches 21; Conservative 0; Mismatches 6;
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; OTHER INFORMATION: Clone ID: 700243862H1
US-09-987-899-5598
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Best Local Similarity 77.8<sup>1</sup>
Matches 21; Conservative
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US-10-242-535A-1095
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RESULT 40

US-10-029-386-1391

Squence 1391, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C.

TITLE OF INVENTION: BXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 1391
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                                                  Query Match 64.4%; Score 17.4; DB 16; Length 292; Best Local Similarity 77.8%; Pred. No. 5e+02; Matches 21; Conservative 0; Mismatches 6; Indels 0;
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.78
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
OTHER INFORMATION: NT HIT: AF156100.1, EVALUE 0.000+00
OTHER INFORMATION: SWISSPROT HIT: P34886, EVALUE 2.100+00
US-10-029-386-1391
                                                                                                                                                                                                                               285 GCTGGTGCACTTAAAGTTATTTATCCT 259
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Job time : 1149.74 secs
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ORGANISM: Homo sapiens
FEATURE:
US-10-085-783A-1095
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BQ319411 MRO-CT045
BJ031520 BJ031520
BX101593 BX101593
AW949936 EST362006
CD691494 EST8017 h
AY402311 Pan trog1
BX955995 DKFZp781F
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BX884672
Mus muscu
EST3 66275
AGENCOURT
HYSME1002
BX403908
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tric025xf
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
                                                                                          January 7, 2005, 10:58:39
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BQ734454
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AY40230
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CK800588
CB828552
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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9b_htc: **

9b_est4: **

9b_est4: **

9b_est6: **

9b_gs81: **
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AZ338890 1M0070G08 N26591 yx91f05.81 CR14361 Forward s BU112231 603002410 BU335623 603496499 BU381772 60385790 AL204986 Tetraodon CL02772 CH216-171 BY592030 BY592030 CR676984 OSUNEe131 AQ654959 Sheared D BQ135922 NF023D01E AQ654959 Sheared D AQ787083 HS 5480 A BF649189 NF023D01E CC551428 GSJNED1G CC51428 GSJNED1G CC55428 BE573142 G01330440 CF924217 DD016D10. BH397370 AG-ND-121	ALIGNMENTS F213103 B666 bp mRNA linear EST 06-NOV-2000 R18501471 NIH_MGC_55 Homo sapiens CDNA clone IMAGE:4070522 5', R213103 F213103 F213103 G1:11106889 SG. Gases Lic & Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; dmanla; Eutheria; Prinates; Catarrhini; Hominidae; Homo. Chases Lic & Med. Gases Lic & Med. TH-MGC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; dmanla; Eutheria; Prinates; Cherdata; Catarrhini; Hominidae; Homo. TH-MGC Metazoa; Chordata; Catarrhini; Hominidae; Homo. Gases Lic & Med. TH-MGC Metazoa; Chordata; Catarrhini; Hominidae; Homo. Datacinal Institutes of Health, Mammalian Gene Collection (MGC) Apublished (1999) Mail: capaber Tarausberg, Ph.D. Mail: capaber remail: nih.gov. Mail: capaber remail: MTC. CONNA Library Preparation: CLONETECH Laboratories, Inc. CONNA Library Preparation: CLONETECH Laboratories, Inc. CONNA Library Arrayed by: The I.M.A.G.E. Consortium (LML) Mail: capaber remail: MA.G.E. Consortium/LINL at: Lipration: MGC clone distribution information can be und through the I.M.A.G.E. Consortium/LINL at: Lipraid: Lipration: MGC clone distribution information can be und through the I.M.A.G.E. Consortium/LINL at: Lipraid: Lipraid: Lipraid: MGE:407052. And Lipraid: MGE:407041 fines And Lipraid: MGE:407052. And Type="mRNM" appeared from call line RNA appeared marrow, Vector: pDNR-LIB (Clontech); Site I: Sfil (ggccccataggcc); Site 2: Sfil Adaptor sequence: And M. F.A.C. G, or T). Average insert size C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range on-2000)
AZ338890 N26591 CK143861 BU112231 BU335623 BU331772 CCNS02N57 CCNS02N57 CCNS02N57 AQ64499 AQ64499 AQ64499 BQ135922 BC135922 CCNS02N57 CCNS02N57 CCNS02N57 CCNS02N57 BCS 1680 CCNS02N57 BCS 1680 CCNS02N57 CCNS02N57 BCS 1680 CCNS02N57 CCNS0	ALIGNMENTS FI NIH_MGC_55 Homo sapiens cDNA ence. 1 GI:11106889 ens (human) ens (human) ens (human) ens (human) ens (secondata; Craniata;) Eutheria; Primates; Catarrhini. tp. (Mgc.nci.nih.gov/. Institutes of Health, Mammalian ed (1999) apbs-r@mail.nih.gov courrement: Array for By: Incyte Genomics, Inc carry Preparation: CLONETECH Lab encing by: Incyte Genomics, Inc carry Arrayed by: The I.M.A.G.E. coursement: Arrayed by: The I.M.A.G.E. carry Arrayed by: The I.M.A.G.E. count in S.G.E. dagerial Income="Homo sapiens" forganism="Homo sapiens" forganism="Homo sapiens" forcatiangeco; forc
๑๐๑๗๓๓๓๓๓๓๓๓๓๓๓๓๓๓๓	IH_MGC_55 I:1110688; (human) tazoa; Che heria; Pr: 0 866) '/mgc.nci itutes of itutes of 1999) rt Straus ement: ATG e
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AUTHORS TITLE

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Query Match

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 304)

N. Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., G.Ylare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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BJ031520 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis CDNA clone XL007ill 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-CT0451-
221100-022-b01&t3=2000-11-22&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 446)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Xenopus laevis
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High quality sequence stop: 6.
Location/Qualifiers
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BJ031520.1 GI:17409728
           Homo sapiens (human)
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                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
I Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LLAM12318 row: p column: 11
High quality sequence stop: 610.

Location/Qualifiers
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/lab_host="DHIOB (phage-resistant)"
/clone_lib="NICHD XGC Emba"
/note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1:
Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo
dr. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 852)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                         Score 19.6; DB 2; Length 866; Pred. No. 1.5e+02;
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Pred. No. 2.4e+02;
0; Mismatches 3; Indels
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:5572858"
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1 Similarity 87.5%;
21; Conservative (
Alto, CA)."
                                                                                                                                           Best Local Similarity 84.6
Matches 22; Conservative
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Gaps

Query Match

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RESULT 3
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AW949936 510 bp mRNA linear EST 01-JUN-2000 EST362006 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 510)
Hegde, P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Bmail: johnq@tigr.org
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|db_xref="taxon:9606"
|clone llb="MAGE resequences, MAGA"
|noce="Vector: pBluescriptSKm"
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100.0%; Pred. No. 2.8e+02;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                          Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
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/dev stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
/ibrary
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Pred. No. 2.8e+02;
0; Mismatches 5; Indels
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Center For Genetic Resource Information
National Institute of Genetics
Mishims, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                           1. .446
/organism="xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL007i11"
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/organism="Homo sapiens"
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Location/Qualifiers
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70.4%;
Best Local Similarity 81.5%;
Matches 22; Conservative
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/locus_tag="HCM1188"
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Best Local Similarity 100.
Matches 19; Conservative
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wanoy, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                            and
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pan troglodytes CD28 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/tiseue type="normal nasopharynx"
/clone lib="human nasopharynx"
/nore="ESTS generated from a normal nasopharynx cDNA
                                                                        Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. Zeng,Y.-X.
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                                                                                              Transcriptional Gene Expression Profile of Human Nasopharynx Unpublished (2003)
Contact: YiXin Zeng
Cancer Center
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                                                                                                                                                                                         Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-2775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="CD28"
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Homo sapiens CD28 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
AY402330
AY402330.1 GI:39758316
                                                                                                                                                                                                                                                                                                                  654 bp mRNA linear EST 01-MAR-2004 nonym: hlcc4) Homo sapiens cDNA clone
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/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 654)
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Seesaarch Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/German/) within the cDNA sequencing consortium of the
German Genome Project.
                                                          Gaps
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This clone (DKRZD781F1075) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANNY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
Wellenreuther,R., et al.)
Unpublished (2003)
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  Length 611;
                                                          Indels
DB 9; Len
2.9e+02;
hes 0;
Query Match 70.4%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 2.5 Matches 19; Conservative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp781F1075"
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DKFZp781F1075_5', mRNA sequence.
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/lab_host="DH10B"
                                                                                                                                                                  287 AATTGAAGTTATGTATCCT 305
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e-mail: abe@rtc.riken.jp
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Mus musculus molossinus
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S Heil,O., Neubert,P., Peters,M., Radelof,U., Schneider,D.,
Schroth,A., Korn,B. and Landgrebe,J.
Schroth,A., Korn,B. and Landgrebe,J.
Schroth,A., Korn,B. and Landgrebe,J.
Xenopus laevis Unidene Set 1 (RZPDLIB No.988)

L Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
RZPD; IMAGS998F228575.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection (amp. resistant) (RZPDLIB
No.998) http://www.rzpd.de/cgi-
bin/products/showlib.pl.cgi/response?libNo-998 RZPDLIB; Xenopus
laevis Unidene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
bin/products/showlib.pl.cgi/response?libNo-988 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
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                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 663)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, W. Murphy, B., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                             Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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BX854672 Kirschner embryo Stl0 14 Xenopus laevis cDNA clone
IMAGp998F228575 ; IMAGE:3516309 5', mRNA sequence.
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/db_xref="taxon:9606"
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/gene="CD28"
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                                               Homo sapiens
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BX854672/c
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Blact Submission

Blact Submission

Blact Submission

Charles Hattori, The Institute of Physical

Bubmitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Subhiro-chou, TBurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: hattoriegsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,

Tel: 81-45-503-911, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

Clones are derived from the mouse EAC library MSMg01. For BAC

library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
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Mus musculus molossinus DNA, clone:MSMg01-053J22.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGD998F228575; IMAGE:3516309"
/tissue_type="pooled embryos (stage 10-14)"
/lab host="DH10B (phage-resistant)"
/clone lib="Kirschner embryo Stl0 14"
/note="Vector: pSC2+; Site 1: Not1; Site 2: Sal1;
Size-selected for average insert size 1: Z kb. Library was constructed and donated by M. Kirschner (Harvard Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Fax: +49 30 32639 111
www.rzpd.de
his clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
SP6, 5' ATTTAGGTGACACTATAG 3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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BAC end Sequences of Library MSMg01
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1. .723
/organism="Mus musculus molossinus"
                                                                                                                                                                                                                                                                         organism="Xenopus laevis"
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-053J22.TJ"
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                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:8355"
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EST 19-OCT-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

1 (bases 1 to 935)

Wing, R., Wenthlbauer, G.J., Close, T.J., Kleinhofe, A., Wise, R.,

Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M.,

Rambo, T., Simmons, J., Penton, R.D., Malatrasi, M., Choi, D.W.,

Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource

for barley genomics: Fusarium infected Morex spike cDNA library

Unpublished (2001)
               Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Genomic / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Igor B. Dawid
cDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15081 row: o column: 22
High quality sequence stop: 721.
High quality Sequence stop: 721.
  National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          935 bp mRNA linear EST 19-OCT (Fusarium infected) Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone HVSME10020K12f, mRNA sequence.
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
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BI950426.1 GI:16292511
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BI950426/c
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray (Dubblished (2000) Contact: John Quackenbush The Institute for Genomic Research 7712 Medical Center Dr., Rockville, MD 20850, USA 712: 301 838 3528 Fax: 301 838 0208
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AGENCOURT 18833449 NICHD XGC Te2N Xenopus laevis cDNA clone
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                 /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                 Score 19; DB 9; Length 723; Pred. No. 2.9e+02; 0; Mismatches 5; Indels
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/mol_type="mRNA"
/dol_xref="taxon:9606"
/dol_xref="taxon:9606"
/clone lib="WAGGE resequences, MAGC"
/note="Vector: pBluescriptSKm"
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Xenopus laevis
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                                                                                                                                                                                     1 GCGCCCCCAATTGAAGTTATGTATCCT 27
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1. .730
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                                                                                                                                                                                                                                                                                                                                                                               AW954205
AW954205.1 GI:8143888
                                                                                                 ch 70.4%;
1 Similarity 81.5%;
22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: johnq@tigr.org
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: Reverse.
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Best Local Similarity
Matches 19; Conservat
                                                                                                 Query Match
Best Local Similarity
Matches 22; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                     AW954205
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CK800588/c
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AW954205
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AUTHORS
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AUTHORS
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CB828552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK(-); Site 1: BCORI; Site 2: Xho1; Plants were grown at the University of Minnesota in the GJ Wuehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified CDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and wing). Plasmid DNA perparations, DNA sequencing and sequence analysis were performed at CUGI (Wing) Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of chara, when the contains a minimum of 100 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically andhored BST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Hordeum vulgare spike EST library HVcDNA0012 (Fusarium infected)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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CLOBB005ZE06 5-PRIME, mRNA sequence.
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Contact: Genoscope
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0
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Pred. No. 3e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                   /organism="Hordeum vulgare" subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
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                     Email: rwing@clemson.edu
Total hq bases = 369
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 913.
Location/Qualifiers
                                                                                                                                                                                                                                                            /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSME10020K12f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCGCCGCAATTGAAGTTATGTATCCT 27
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                                                                                                                                                                                                                                                                                                                                           /tissue_type="Spike"
/lab_host="TJC121"
                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX403908.2 GI:46957179
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Best Local Similarity 81.5%;
Matches 22; Conservative
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  7ax: 864 656 4293
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AUTHORS
TITLE
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COMMENT
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/tissue type="NEUROBLASTOWA"
/close lib="Homo sapiens NEUROBLASTOWA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotL-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB828552 521 bp mRNA linear EST 16-MAY-200
LjNEST87h1r Lotus japonicus nodule library 5 and 7 week-old Lotus
corniculatus var. japonicus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 521)
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                   This sequence belongs to sequence cluster 6542.f
For more information about this cluster, see
http://www.genoscope.cns.ff/cdna?s=CLOBB005ZE06RP1&c=6542.f.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lib="Lotus japonicus nodule library 5 and 7
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    .521
    /organism="Lotus corniculatus var. japonicus"

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Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
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                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'clone="CL0BB005ZE06"
                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity
Matches 20; Conserv
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Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreacea;
(bases 1 to 815)
Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Mard,M. and Dean,R.A.
Characterization of the protein processing and secretion pathways in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="mycelia" /clone_lib="T.reesei mycelial culture, Version 3 april" /note="Teesei mycelial site_l: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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Hypocrea jecorina cDNA clone tric025xf21, mRNA sequence.
CF870869
tric025xf21 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone tric025xf21, mRNA sequence.
CB901075
                                                                                                                                                                                           Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocreacea; Hypocreacea; Hypocrean; Everan; P. Bassi; Brown, D. B., Dankmeyer, L., Dean, R., Diener, S., Dunn-Coleman, N. S., Goedegebuur, F., Houtek, T. D., England, G.J., Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C., Ollvares, H.A., Teunissen, P. J., Yao, J. and Ward, M. Transcriptional regulation of blomass-degrading enzymes in the filamentous fundus Trichoderma resea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.9%; Score 18.6; DB 6; Length 815; Best Local Similarity 84.0%; Pred. No. 4.7e+02; Matches 21; Conservative 0; Mismatches 4; Indels
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                                                                                                                                             Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
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FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
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Location/Qualifiers
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Fax: (650) 621-7817
Email: Pforeman@genencor.com
                                                                                                 CB901075.1 GI:30115733
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/lab host="UMN07 or DH5a"
/clone_lib="WG5-ZmaysF (JM107 adapted methyl filtered)"
/clone_lib="WG5-ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
fractionated using sephadex. The resulting fragments were
fraction of 8 and 3 Xb and were cloned into the vector
(.x/y reads in M13mpl9, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a. "
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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bz06d07.gl WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone hz06d07 5', genomic survey sequence.
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Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martienssen, R.A. Genomic shorgun sequences from Zea mays (methyl-filtered) Unpublished (2002)
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                                                                                               Query Match 68.9%; Score 18.6; DB 6; Length 521; Best Local Similarity 84.0%; Pred. No. 4.5e+02; Matches 21; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: W. Richard McCombie
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hccombie@cshl.org
Seg primer: -21M13UnivRev
Class: shotgun
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/cultivar="B73"
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Location/Qualifiers
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                         strain R7A."
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Gaps . 0 EST 31-OCT-2003

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BP512240
831 bp mRNA linear EST 16-SEP-2003
BP512240 Hydra magnipapillata cDNA library Hydra magnipapillata
CDNA clone hmp_05691, mRNA sequence.
BP512240
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OGLAO86TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0718P03,
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(Dases 1 to 919)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                   Hayakawa, S., Hwang, J.S., Nishimiya-Fujisawa, C., Ogura, A., Ikeo, K., Fujisawa, T. and Gojobori, T. Hydra EST project Unpublished (2003)
                                                                                                                                                                                                                        Hydra magnipapillata
Hydra magnipapillata
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
1 (bases 1 to 831)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-981-6847(ex.6898)
Fax: 81-55-981-6848
Email: jhwangelab.nig.ac.jp, URL:http://www.cib.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Jung Shan Hwang
Center for Information Biology and DNA Data Bank of Japan
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:6085"
/clone="hmp_05691"
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/dew stage="adult budding stage"
/clone_lib="Hydra magnipapillata cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.9%; Score 18.6; DB 5; Length 831; Best Local Similarity 84.0%; Pred. No. 4.7e+02; Matches 21; Conservative 0; Mismatches 4; Indels
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/mol_type="mRNA"
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    132 GGACTCAATTGAAGAGATGTATCCT 156
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CG303571.1 GI:34217785
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Contact: Cathy Whitelaw
                                                                                                                                                                                         BP512240.1 GI:34778373
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BOHQC78TF BOHQ Brassica oleracea genomic clone BOHQC78, genomic
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Brassica oleracea
Brassica oleracea
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 818)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BOHQC78TR
                                                                                                                                                                                                                          /dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
                                                                                                                                                                                                                                                                                              /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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/clone="BOHQC'8"
/clone=lib="BOHQ"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
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                                                                                                                        /organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="OM6a"
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/strain="TO1000DH3"
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/clone="tric025xf21"
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Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph deamoncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers
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Fax: 301-838-0208
                                                                                                      1. .815
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BH463620
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AUTHORS
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BH463620
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Gaps

GSS 29-SEP-2000

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (base 1 to 628)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Miederhausern, A. and Wright, D., Weise, R., Mouse whole genome scaffolding with paired end reads from 10kb
                                   42318890 628 bp DNA linear GSS 29-SEP-200
IMO070GO8F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                             clone UUGC1M0070G08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84112, 0.57
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 10000 Std Error:
Plate: 0070 row: G column: 08
Seq primer: CGTFGTAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 628.
Location/Qualifiers
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/clone="UUGC1M0070G08"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CAATTGAAGTTATGTATCCT 27
                                                                                                     AZ338890.
AZ338890.1 GI:10412612
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95.0%;
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Best Local Similarity 95.0
Matches 19; Conservative
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AUTHORS
RESULT 25
AZ338890
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Submitted (01-CTT-2001) Genoscope - Centre National de Sequencage :

By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

(bases 1 to 486)

(chases 1 to 486)

Locath.C.W. Brey.P.T., Ke,Z. and Collins,F.H.

Direct Submission

Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr.

This clone is from an A. gambiae BAC library provided by F.H.

Collins and sequenced by Genoscope in collaboration with the laboratory of Biochem. and Biol. Molec. of Insects, Institut
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Anopheles gambiae
Eukaryota, Merazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                 /organism="Zea mays"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="texon:4577"
/clone="ZMWBMa0718P03"
/clone="ZMVBMa0718P03"
/note="Voctor: PBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                     Length 919;
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/clone="18E09"
/clone_lib="NotreDamel"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="genomic DNA"
/strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                         PATGIAICCI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                            37 GGCCACCATATAAGTTATGTATCCT 61
                 Seg primer: TP
Class: sheared ends.
Location/Qualifiers
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Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
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95.0%;
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Best Local Similarity
Matches 19; Conserva
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Matches 21; Conserv
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gilf4[p1]14[p4]he129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculs C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 5.7e+02;
0; Mismatches 1; Indels C
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Gaps

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/organizami- ostrus yaring
/mol type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="ch85710(4")
/db_bost="2"
/lab_bost="DH10B"
/lab_bost=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 768)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Curr. Biol. 12 (22), 1965-1969 (2002)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 999)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Brogers,J. and Bradley,A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
Location/Qualifiers

1. .999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BU112231 768 bp mRNA linear EST 25-NOV-2002
603002410F1 CSEQCHL14 Gallus gallus cDNA clone ChEST10c4 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 68.1%; Score 18.4; DB 9; Length 999; I Similarity 95.0%; Pred. No. 6e+02; 19; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN246d22"
/clone_lib="MHPN"
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BU112231.1 GI:25316259
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simon Hubbard
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BU112231/c
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yx91f05.sl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:269121 3', mRNA sequence.
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Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN246d22, genomic survey sequence.
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 720)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
High quality sequence stops: 424
Source: IMAGE Consortium, LiNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.1%; Score 18.4; DB 7; Length 720; 95.0%; Pred. No. 5.8e+02; ive 0; Mismatches 1; Indels
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CR143861.1 GI:49891738
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="GDB:3878763"
/db_xref="taxon:9606"
/clone="IMAGE:269121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CAATTGAAGTTATGTATCCT 27
                                                                                                                                                                             N26591.1 GI:1140939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.03
Matches 19; Conservative
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                  N26591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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CR143861
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JOURNAL
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      RESULT 26
N26591/c
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KEYWORDS
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KEYWORDS
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//dev stage="36"
//dev stage="36"
//done_lib="CSEQCHN5"
//clone_lib="CSEQCHN5"
//clone_lib="CSEQCHN5"
//note="Organ: trunks; Vector: pBluescript II KS(+);
//site_l: BcoRl; Site_2: Not!; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not! adapters, digested with
EcoRl, size-selected, and cloned into the Not! and EcoRl
compatible sites of a custom modified McS of the
pBluescript (KS+) vector: The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1995): 791, except that a significantly longer
reannealing hybridization was used."
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                                                                                                                                                                                                 BU381772 825 bp mRNA linear EST 28-NOV-2002
603855790F1 CSEQCHN75 Gallus gallus cDNA clone ChEST859c24 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

I (bases I to 825)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Curr. Biol: 12 (22), 1965-1969 (2002)
22335534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 01612008930
Fax: 01612366490
Email: Simon Hubbard@unist.ac.uk.
Location/Qualifiers
1, 825
//organism="Gallus gallus"
//mol_type="mRNA"
/ strain="Mhite Leghorn, Hisex"
/db xrefe"taxon:9031"
/clone="ChEST85924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Po Box 88, Manchester, M60 1QD, UK
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        4 GCCGCAATTGAAGTTATGTATCC 26
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                                     79 GCTGCAATGGAAGTTACGTATCC
                                                                                                                                                                                                                                                                                                           BU381772.1 GI:25889773
                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simon Hubbard
                                                                                                                                                                                                                                                             sequence.
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BU381772/c
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DEFINITION
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CNS02N5T
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/clone lib="CSECTRNGS"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site_1: BCORI; Site_2: Noti; Fils normalized library was
constructed from imilion independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand caction, double-stranded CDNA
was blunted, ligated to Notl adapters, digosted with
ECORI, size-selected, and cloned into the Notl and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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Gallus gallus
Gallus gallus
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
1 (Bases I to 788)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong; W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehenaive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           BU335623 788 bp mRNA linear EST 28-NOV-2002 603496949F1 CSEQCHN65 Gallus gallus cDNA clone ChEST408a13 5', mRNA
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Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgcagccccggatccgaaaaaag] [5'aattcttttttttggatccgggctgcacgc]"
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University of Manchester Institute of Science and Technology
(UMIST)
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                                                                                                                                        Query Match 67.4%; Score 18.2; DB 5; Length 768; Best Local Similarity 87.0%; Pred. No. 7.3e+02; Matches 20; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole embryo"
/dev_stage="10"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .788
/organism="Gallus gallus"
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Email: Simon.Hubbard@umist.ac.uk.
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/clone="ChEST408a13"
                                                                                                                                                                                                                                                                                                        GCTGCAATGGAAGTTACGTATCC 174
                                                                                                                                                                                                                                                  4 GCCGCAATTGAAGTTATGTATCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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BU335623.1 GI:25843624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
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AUTHORS
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COMMENT
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                                                                                  ORIGIN
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us-09-786-502a-7.rst

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Crammantaria nucuenta; Scutrognachi; Muridae; Murinae; Mus. Crammantaria; nucuenta; Concerta; Suzuki, H., Yadachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Chothia, C., Corbani, L.B., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Ghothia, C., Godik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Paran, W.J., Pertea, G., Pesole, G., Perosole, G., Pervosky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachantan, S., Shraeider, C., Sepule, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R., Magner, L., Wahlested, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Kawai, J., Atakawa, T., Fukuda, S., Hara, A., Hashizume, W., Inctan, K., Inch, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Itoh, M., Kagawa, T., Pukuda, S., Hara, Y., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 bp mRNA linear BST 15-DEC-2002 BYS92030 RIKEN full-length enriched, adult inner ear Mus musculus CDNA clone F930021E21 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
A physical map of the xenopus tropicalis genome Unpublished (2003)
Contact: Richard K Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.4%; Score 18.2; DB 9;
87.0%; Pred. No. 7.8e+02;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus tropicalis"
/mol type="genomic DNA"
/strain="Nigerian frog"
/db_xref="teaxon:8364"
/clone="CH216-1718"
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Best Local Similarity 87.01
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                         1, .1329
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BY592030/c
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neoperygii, Taleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Sautin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish retraodon nigroviridis
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                                                                                                                                                                                                                                                                                                           Rocet Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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//mol type="genomic DNA"
/db_xref="taxon:99883"
/clone="150J10"
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                                                       AL204986.1 GI:7863805
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: I column: 20
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Fax: 520 621 9288
Email: http://genome.arizona.edu
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/dev_stage="3_week"
/lab_host="DH10B"
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AQ654959.1 GI:5148145
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                                                                                                                                                                      Taylogus, and and an are contact. Group, RIKEN Genomic Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Vokohama Institute of The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 7el: 81-45-503-9222 Fax: 81-45-503-922 Fax: 81-45-503-92 Fax: 81-45-503
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Oryża sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                              Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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/clone="F930021E21"
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/strain="C57BL/6J"
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Trypanosoma.

Tr
Ehrhartoideae; Oryzeae; Oryza.

1 (Dases 1 to 508)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Jantasuriyarat,C., Loderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Arizona Genomics Institute
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/note="Vector: SBluescript II KS +; Site_1: EcoRI; Site_2:
Xho1; 24 hrs after innoculation with Rice Blast (70-15)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 22-JUN-1999
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Sheared DNA-21K22.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-21K22, genomic survey sequence.
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
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/organism="Oryza sativa (japonica cultivar-group)"
/orlivar="MRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
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80.8%; Pred. No. 8.7e+02;
ive 0; Mismatches 5; Indels
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Gaps

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In Journal 10 599)

E 1. Sayed, M., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93
Library for gene discovery and sequence-ready map construction
Library for gene discovery and sequence-ready map construction
Cher GSS: RPCI93-DpnII-28M12.TJ
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Trypanosoma brucei"
// prognism="Trypanosoma brucei"
// mol type="genomic DNA"
// strain="TrEU927/4 GuTat 10.1"
// db xref="taxon:5691"
// clone="REC193-DpnII-28M12"
// clone="REC193-DpnII"
// note="Vector: pacce.6; Site_1: Bam HI; Site_2: Bam HI;
// note="Vector: pacce.6; Site_1: Bam HI; Site_2: Bam HI;
// note="Vector: pacce.6; Site_1: Bam HI; Site_2: Bam HI;
// note="Vector: pacce.6; Site_1: Bam HI; Site_2: Bam HI;
// note="Vector: pacce.6; Site_1: Bam HI; Site_2: Bam HI;
// constructed for The Institute for Genomic Research by
// Bohui Zhao in Pieter do Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
// brucei TREU927/4 GuTat 10.1 agarose embedded DNA was
// partially digested with a combination of Eco RI and Eco
methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII
// segment). High molecular weight fragments were ligated in
// paccelively. The average insert size is 141 KD. Total
days. Cells were induced six days after subculture" /clone lib="Elicited cell culture" /note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ644499 11-28M12.TV RPC193-DpnII Trypanosoma brucei genomic clone RPC193-DpnII-28M12, genomic survey sequence.
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Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
page: http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                              Query Match 66.7%; Score 18; DB 5; Length 562; Best Local Similarity 80.8%; Pred. No. 8.8e+02; Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-minichromosomal genome."
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AQ644499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Court The Sucarce of the Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 bp mRNA linear EST 23-APR-2002 NF023D01EC1F1012 Elicited cell culture Medicago truncatula cDNA clone NF023D01EC 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
   DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tcb/mdb/tbdb/. Seq primer: M13-Reverse Class: shotgun.
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/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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80.8%; Pred. No. 8.8e+02;
cive 0; Mismatches 5; Indels
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/mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                       /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927/4 GUTat 10.1"
                                                                                                                                                                                                                                                                                                                                                                                  db xref="taxon:5691"
/clone="Sheared DNA-21K22"
/clone_lib="Sheared DNA"
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Medicago truncatula
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BQ135922
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/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
dev_stage="Cell suspensions were subcultured every 14
dev_stage="Cells were induced six days after subculture"
/clone lib="Elicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to Soug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bhrhartoideae; Oryzae, Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae, Oryza.

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Jantasuriyarat,C., Lu,G.,Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB651428 119 bp mRNA linear EST 08-APR-2003 OSJNEb16G03.f OSJNEb Oryza sativa (japonica cultivar-group) cDNA clone OSJNEb16G03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research Unpublished (2000)
                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                  NF055A06EC1F1039 Elicited cell culture Medicago truncatula cDNA clone NF055A06EC 5', mRNA sequence.
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80.8%; Pred. No. 8.9e+02;
ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7380
Email: radixon@noble.org
Email: radixon@noble.org
Insert Length: 625 Std Error: 0.00
Plate: 055 row: A column: 06
Seq primer: TCACACAGGAAACAGGTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Medicago truncatula"
/mol type="mkm4"
/mol type="mkm4"
/clore="NP055A06EC"
                                                                                                                                                Medicago truncatula (barrel medic)
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Best Local Similarity 80.8
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Dixon RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3818
Fax: (206) 616-3818
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 1056 row: C column: 3
Seg primer: T7
Class: BAC ends
High quality sequence stop: 621.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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genomic clone Plate=1056 Col=3 Row=C, genomic survey sequence.
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: $20 626 3967
Fax: $20 621 9288
Email: http://genome.arizona.edu
PCR PRimers
FORWARD: gda aaa cga cgg cca gtg
BACKWARD: gga aac agc rat gac cat g
Plate: 16 row: G column: 03
Seq primer: gfa aaa cga cgg cca gtg.
BACKWARD: gga aac agc rat gac cat g
Plate: 16 row: G column: 03
Seq primer: gfa aaa cga cgg cca gtg.
BACKWARD: gga aac agc rat gac cat g
Plate: 16 row: G column: 03
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Search completed: January 7, 2005, 12:37:39 Job time : 1617.95 secs

246 GCAGCGCATTCGAAGGTGTGTATCC 271

8 8

1 GCGCCGCATTGAAGTTATGTATCC 26

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Ouery Match 66.7%; Score 18; DB 6; Length 719; Best Local Similarity 80.8%; Pred. No. 9.1e+02; Matches 21; Conservative 0; Mismatches 5; Indels

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; Search time 228.421 Seconds (without alignments) 689.440 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	AAA10271	ABA92025	ADK98583	AAT27650	AAX90349	AAQ21167	AAT36257	AAT14707	AAV63445	AAV81203	AAA50581	AAZ29325	AAS03175	ABA99035	ADD25537	AD131990	AD049343	AAN90607	AAT27652	AAT27651	AAL49546
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Substantial function. The cytoplasmic domain directs the function of the function receptor and is generally the cytoplasmic domain of a molecule which functions as a transducer of a mammalian immune response in the presence of an MRC (major histocompatibility complex)-peptide complex or costimulatory factor. Examples of cytoplasmic domains that may be costimulatory factor. Examples of cytoplasmic domains that may be invention in the present invention include the T-cell receptor gamma-chain cytoplasmic domain and the CD28 cytoplasmic domain. In a method of the invention, an expression vector encoding the fusion receptor is transduced into primary T-lymphocytes obtained from the patient to be treated. The transduced lymphocytes are returned to the patient where they secrete interleukin-2 (IL-2) and proliferate in response to PSMA-positive cells. The resulting cytotoxic lymphocytes specifically lyse cells expressing PSMA and can thus be used to target PSMA-positive tumour cells useful for the treatment of prostate cancer and other cancers that express PSMA. Sequences AAA10270 represent PCM primers used in an express PSMA. Sequences analysis of the present invention to amplify cancer that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a gene encoding a fusion
between the PSMA-scFv and the cytoplasmic domain, such that both retain substantial function. The cytoplasmic domain directs the function of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention to amplify cDNA encoding the cytoplasmic and transmembrane domains and part of the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain of human CD28. This was used to construct a gene receptor comprising the PSMA-scFv and the CD28 fragment
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Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other;

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100.0%; Score 30; DB 3; Length 30; 100.0%; Pred. No. 0.00094; ive 0; Mismatches 0; Indels
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ABA92025 standard; DNA; 30 BP RESULT 2

(first entry) 23-MAY-2002 ABA92025;

Human CD28 cDNA downstream PCR primer.

CD28; T cell; receptor; human; antitumour; immunostimulant; cancer; therapy; neuroblastoma; melanoma; sarcoma; small lung carcinoma; brain tumour; disialoganglioside GD2; imaging; PCR; primer; 88.

Homo sapiens

US2002018783-A1.

14-FEB-2002.

97US-00940544. 97WO-US004427 30-SEP-1997; 20-MAR-1997;

SADELAIN M. CHEUNG N V. KRAUSE A. GUO H. (KRAU/) (GUOH/) SADE/) CHEU/)

Guo H; Krause A, Cheung NV, Sadelain M,

WPI; 2002-239251/29.

New fusion protein, useful for inducing host immune response, comprises variable region of light chain of an antibody linked to variable region of antibody, CD28 receptor signaling domain and transmembrane domain.

Example 3; Page 4; 9pp; English

The present sequence is that of a downstream primer, used with the

co thuman T cell surface receptor CD28 cDNA. The amplification of a segment of human T cell surface receptor CD28 cDNA. The amplified segment encodes correctly contained bacD28, and the transmembrane and the cytoplasmic domains. Plasmid pbsCD28 was used as template. The 5' primer cytoplasmic domains. Plasmid pbsCD28 was used as template. The 5' primer contains an Not1 site, while the 3' primer contains a BamHI site, and the trenviral vector SFG. A cell-surface molecule capable of CD28 signalling cretroviral vector SFG. A cell-surface molecule capable of CD28 signalling constructed. This comprised the antigon-binding site of a GD2-specific antibody and the transmembrane and signalling domains of the CD28 molecule. This is an example of fusion proteins of the invention comprising such fusion proteins exhibit enhanced survival when comprising such fusion proteins exhibit enhanced survival when response to cells, particularly tumour cells which express the anti-GD2 sefv are useful for treatment of melanomas, and head in contain and anti-GD2 sefv are useful for treatment of melanomas. ö neuroblastomas, small lung carcinoma, sarcomas and brain tumours that express GD2 as a surface antigen. Cells expressing the fusion proteins of the invention can also be used for in vitro purging of stem cells or bone marrow and for in vivo targeting of tumour cells and other antigen-Length 30; Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other; Score 30; DB 6; Pred. No. 0.00094; 100.0%; bearing cells for imaging

Gaps .. 0 0; Indels 0; Mismatches Query Match
Best Local Similarity 100.0

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ADK98583 standard; cDNA; 454 BP ADK98583; ADK98583/c RESULT 3

03-JUN-2004 (first entry)

Human immune response associated protein IRAP-11 cDNA.

cytostatic; neuroprotective; antiparkinsonian; hepatorropic; cerebroprotective; antiinflammatory; nootropic; vasotropic; arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease; Parkinson's; Crohn's; gene therapy; human; ss; gene. immune response associated protein; IRAP; antiarteriosclerotic;

WO2004020593-A2

11-MAR-2004

2002US-0407561P. 2002US-0410178P. 2002US-0410571P. 18-OCT-2002; 2002US-0419906P. 25-OCT-2002; 2002US-0421445P. 26-AUG-2003; 2003WO-US026988 30-AUG-2002; 11-SEP-2002;

(INCY-) INCYTE CORP.

Ramkumar J, Swarnakar A, Elliott VS, Hafalia AJA, Richardson Lee SY, Lindquist EA, Marquis JP, Chawla NK, Khare R, Becha

WPI; 2004-239178/22.

N-PSDB; ADK98548

New isolated immune response associated proteins (IRAP) polypeptide and

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The invention relates to a novel isolated immune response associated protein (IRAP) comprising any of 35 fully defined sequences given in the specification. The polypeptide of the invention demonstrates antiarteriosclerotic, cytosciatic, neuroprotective, antiparkinsonian, hepatotropic, cerebroprotective, antinflammatory, nootropic and vasotropic activities and may be useful for treating a disease or condition associated with decreased expression or overexpression of functional immune response associated proteins, while the antibody is expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease and Crohn's disease.
polynucleotide, useful for diagnosing and/or treating disorders with aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i independent cytotoxic T lymphocytes useful in tumour or viral therapy are activated by adhesion to antigen displaying cells.
                                                                                                                                                                                                                                                                                                      Furthermore, the molecules of the invention may be utilised during gene therapy procedures. The current sequence is that of a himan IRAP cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is a BamHI-SalI fragment encoding a chimeric receptor, composed of the extracellular region (XR) of CD2, fused via the transmembrane region (TM) of CD28 to the intracellular region (IC28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chimeric receptor; CD2; extracellular domain; CD28; transmembrane region; intracellular domain; retrovirus; vector; packaging cell culture; gene transfer; LFA-3; selective activation; cytocoxic T-lymphocyte; antitumour; immnotherapy; cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 20.4; DB 12; Length 454; 95.5%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 454 BP; 109 A; 142 C; 105 G; 98 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 31;
0; Mismatches
                                                                      5; SEQ ID NO 46; 207pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 54-55; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 CGTGTCAGGAGCGATAGGCTGC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT27650 standard; cDNA; 875 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TARG-) TARGETED GENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-US014171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00480577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00332993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD2-CD28 chimeric receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feldhaus AL, Jones LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-239497/24.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virucide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9613584-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1996.
                                     and stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT27650;
                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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cD28. TM and IC28 coding sequences of human CD28 (bp 556-767) are amplified by PCR from human CD28 cDNA, and the XR of CD2 (bp 1-627) is amplified by PCR from human CD2 cDNA. The sequences are closed to form Dlasmid pSKcytoCD28. The second of HYTR-CMV-Cat to form HYTR-CMV-Cat to packaging cell culture to give a stable PA317 cell line producing high titers of infectious retrovirus particles, which are then used to infect "-1ymphocytes. The resulting cytotoxic T-1ymphocytes (CTLS) are selectively activatable, and have a lessened dependence on helper T-1ymphocytes (TH cells) and/or growth factors. The chimeric receptor binds to the CD2 ligand (leukocyte function-associated antigen-3 or LRA-3), but 1028 transmits the proliferative signal of CD28. The CTLS mediate lysis of a target cell bearing a cognate antigen, and are useful in directed
                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for inhibiting the expression c CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX9028 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. The present sequence represents a DNA sequence of the human CD28 gene from the present invention
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduces CD28 gene expression in T cells - for diseases, e.g. graft vs. host disease, septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2; immune system mediated disease; gamma-interferon; IL-8; ss.
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                             Score 20.4; DB 2; Length 875;
Pred. No. 35;
0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                 cancer immunotherapy, and in treatment of viral infections
                                                                                                                                                                                                                                                                                                         Sequence 875 BP; 277 A; 188 C; 202 G; 208 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      868 cerercadadedaradecrec 847
                                                                                                                                                                                                                                                                                                                                                                                                                                 9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 1C, 45pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CD28 gene DNA sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX90349 standard; DNA; 1064 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00387041.
                                                                                                                                                                                                                                                                                                                                               ch 68.0%;
|| Similarity 95.5%;
| 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00529878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligo: nucleotide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shock, psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-384228/38.
P-PSDB; AAY24470.
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAMR/) TAM R C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Reduction; T cell; CD28; gene expression; treatment; immune system; disorder; graft versus host disease; septic shock; viral disease; psoriasis; type I diabetes mellitus; thyroiditis; sarcoides; multiple sclerosis; uveitis; rheumatoid arthritis; systemic lupus erythematosus; inflammatory bowel disease; triplex forming; antisense; oligonucleotide; ss.

Location/Qualifiers 100. .762 /*tag= a

WO9624380-A1

15-AUG-1996

sapiens

AAT36257 standard; cDNA; 1514 BP.

(revised)
(first entry)

25-MAR-2003 15-APR-1997

AAT36257;

Human CD28 cDNA.

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AAT36257/c
                                               RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A library of recombinants having inserts greater than 0.8kb in size was prepared in the piH3M vector (see AAQ21166) from 1 microgram of polyA (plus) RNA isolated from the human lymphoblastic cell line JT. The library was screened for CD28 CDNA clones which were isolated using the antibody enrichment method (see e.g. AAQ21164 or AAQ21165). After the third transfection, COS cells were panned with a specific anti-CD28 Ab. A Hirt supernatant was generated and transfected into E.coli. DNA was prepared from the resulting colonies and transfected into COS cells. Surface expression of CD28 antigen was detected in 3 of the 8 transfected positives by indirect immunofluorescence. The cDNA insert from one of the gostilue clones was sequenced. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New CD53 cell surface antigen and DNA encoding it - for immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning technique; cell surface antigen; immunodiagnosis; tumour;
                                                 ö
    DB 2; Length 1064;
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                                               Indels
                                               Ξ,
68.0%; Score 20.4; C
95.5%; Pred. No. 36;
:ive 0; Mismatches
                                                                                                                  316 CGTGTCAGGAGCGATAGGCTGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          Human CD28 antigen coding sequence.
                                                                                       CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "CD28"
100. .153
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 7; 160pp; English
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AAQ21167 standard; DNA; 1514 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aruffo A, Amiot M;
                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP.
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                                               Conservative
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P-PSDB; AAR20805.
                        Local Similarity
tes 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1990;
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                                                                                                                                                                                                                                                                                                                           25-MAR-2003
21-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                       σ
                                                                                                                                                                                                                                                                                     AAQ21167;
    Query Match
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                          Best Loca
Matches
                                                                                                                                                                                              AAQ21167/
AAQ2167/
AAQ21167/
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AAQ21167/
AAQ21-
AAQ21167/
AAQ21-
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Antisense or triplex forming oligonucleotides which target sites within the present sequence, the CD28 cDNA, reduce T cell CD28 gene expression, useful in the treatment of CD28 mediated diseases, particularly immune system disorders, e.g. graft versus host disease, septic shock, viral disease, psoriasis, type I diabetes mellitus, thyroiditis, sarcoides, multiple sclerosis, uveitis, rheumatoid arthritis, systemic lupus erythematosus, inflammatory bowel disease, etc. Reducing CD28 expression may reduce the effects of antigenic stimulation of CD28 positive T cells, with a consequent reduction in cytokine release. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                              Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 1B; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT14707 standard; cDNA; 1514 BP
                                                   95US-00387041.
95US-00529878.
96WO-US001507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 68.0%;
1 Similarity 95.5%;
21; Conservative
                                                                                                                                   (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                 WPI; 1996-384228/38.
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       shock, psoriasis,
                                                                                                                                                                                                                                                                             P-PSDB; AAW02131.
                                                   09-FEB-1995;
18-SEP-1995;
05-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
AAT14707/c
ID AAT1470
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Gaps

; 0

Score 20.4; DB 2; Length 1514; Pred. No. 37; 0; Mismatches 1; Indels 0;

Query Match
Best Local Similarity 95.5%;
Matches 21; Conservative

766 cerercaedaecearaecrec 745

CTTGTCAGGAGCGATAGGCTGC 30

σ

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AAT14707;

Key

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This nucleotide sequence comprises human CD28 cDNA. The cDNA was isolated from HPB-ALL human T-cell tumour cells using a novel method for cloning convaint the memmalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expression antigen by adhesion to an antibody-coated substrate. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell. It has been used to clone genes cloning as such as CD1-53, ICAM, LFA-3, FCRIA, FCRIB, TLisA, and Leu8 (see AAW80440-55). CD28 polypeptide (see AAW80442) has been expressed in transfected COS cells. The purified genes and proteins are useful for immunodiagnostic and immunotherapeutic applications, including the disposses and treatment of immuno-mediated infections, diseases, and disorders of animals, including humans. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cloning vector and poly:linker - based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20.4; DB 2; Length 1514; Pred. No. 37; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                 CD28; cell surface antigen; human; lymphocyte; cloning; ss
                                                                                                      Location/Qualifiers
100. .762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 7A-B; 75pp; English.
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ID AAV81203 standard; cDNA; 1514 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocyte antigenic sequences
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89US-00379076.
90US-00498809.
90US-00553759.
92US-00983647.
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95.5%;
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154. .759
/*tag= c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seed B, Aruffo A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW80442.
Human CD28 cDNA
                                                                      sapiens
                                                                                                                                                                                                                                                                                                                         21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1990;
13-JUL-1990;
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                                                                                                                                                            sig_peptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obtd. by constructing an expression library in COS cells using cDNA decived from human T-cell tumnour line HPB-ALL and vector pit3M (see also AAT14705), and panning of the library using antibody-coated plates. This immunoselection cloning method, developed to clone genes for cell surface antigens of human lymphocytes (see also AAT14703.04 and AAT14706-26), has general appln. Cell surface antigens are obtd. for diagnostic and therapeutic use. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A cDNA clone (AAT14707) codes for human CD28 antigen (AAR91433). It was
                                                                                                                                          Cell surface antigen; cloning; immunoselection; immunotherapy; therapy; diagnosis; vector; piH3M; CD28; COS; T-lymphocyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning of cDNA encoding cell surface antigen - useful for isolation of diagnostic and therapeutic proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1514 BP; 404 A; 359 C; 337 G; 414 T; 0 U; 0 Other;
                                                                                                                                                                                                                               Location/Qualifiers
100. .762
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89US-00379076.
90US-00553759.
92US-00983647.
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100. .153
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/*tag= c
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(first entry)
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(first entry)
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                                                                                                        Human CD28 cDNA
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                                                  25-MAR-2003
30-OCT-1996
                                                                                                                                                                                                Homo sapiens
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07-JUN-1999
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Query Match Matches

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RESULT 9
AAV63445/

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CD28; cell surface antigen; human; immunoselection; panning; immunodiagnosis; diagnosis; immunocharapy; gene therapy; immune disorder; infection; asthma; immune-complex disease; amyloidosis; munitiple sclerosis; parasitic disease; ss.

Location/Qualifiers

sapiens.

Ношо

/*tag= P /*tag= b 154..759

sig_peptide

/*tag=

US6111093-A 29-AUG-2000

Human cell surface antigen CD28 cDNA.

19-DEC-2000 (first entry)

AAA50581;

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This nucleotide sequence comprises human CD28 cDNA. The cDNA was isolated from HPB-ALL human T-cell tumnour cells using a novel method for cloning cDNAs from mammalian expression libraries. The method is babyd or transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell. It has been used to clone genes surface membrane of a eukaryotic cell. It has been used to clone genes (see AAV81198-220) encoding cell surface antigens such as CD1a, CD1b, CD1c, CD2, CD5, CD7, CD13, CD14, CD16, CD19, CD20, CD2, CD26, CD27, CD44, CD53, ICAM, LFA-31, FerRia, FerRia, TRAIS and Leus (see AAW86188-62, AAW89151-52 and AAW80451). CD40 cDNA (see AAW81198) is specifically claimed. CD28 polypeptide (see AAW88451) has been expressed in
                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell surface antigens, constructing cDNA libraries, expressing vectors for expression in eukaryotic cells or their fragments.
                                        cell surface antigen; human; T cell antigen; T lymphocyte;
                                                                                                                                                                                                                                                                                                                         Stengelin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.0%; Score 20.4; DB 2; Length 1514; 95.5%; Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                        , Stamenkovic I, Ste
Simmons D, Aruffo A;
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 7A-B; 79pp; English
                                                                                                                                                                                                                                                                                                                        Camerini D,
Allen J, S
                                                                                                                                                                                                                                      88US-00160416.
89US-00379076.
90US-00498809.
90US-00553759.
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154. .759
/*tag= c
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.153
(first entry)
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Lauffer L,
                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-069813/06
                                       CD28; cell surface cDNA library; ss.
                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW88451
                    Human CD28 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transfected COS
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13-JUL-1990;
01-DEC-1992;
10-MAY-1999
                                                                        Homo sapiens
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                                                                                                                                                                           US5849898-A
                                                                                                                        sig_peptide
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88US-00160416. 89US-00379076. 90US-00498809. 90US-00553759.

23-MAR-1990; 01-DEC-1992;

92US-00983647

(GEHO) GEN HOSPITAL CORP.

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Stamenkovic I, Seed WPI; 2000-586382/55. P-PSDB; AAY96128

98US-00181612

28-OCT-1998;

25-FEB-1988

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                                                                                                                                                                                                                                                                                                                             (CSA) CD28 (See AAY96128). The CDNA was derived from a human T-cell tumour line HPB-ALL CDNA library using a new method for cloning CSA tumour line HPB-ALL cDNA library using a new method for cloning CSA colls. The method is based upon transient expression of CSA in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to (panning on) an antibody-coated substrate such as a culture dish. The predicted amino acid sequence of CD28 suggests an integral membrane protein with a single membrane-spanning hydrophobic domain terminating in a 41-amino acid cytoplasmic domain. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for diagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, diseases, and disorders in animals, including humans. These disorders include asthma,
                                                                                                                                                                                                                                                                                              The present sequence is that of cDNA encoding human cell surface antigen
Isolated nucleic acid molecule encoding the CD19 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .mmune-complex disease, amyloidosis, parasitic diseases or multiple
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                                                                                                                                                                                                                   Example 3; Fig 7A-B; 75pp; English.
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Best Local Similarity 95.5%;
Matches 21; Conservative
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                                                                                                                                        diseases
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Gaps

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21; Conservative

Matches

Local Similarity

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RESULT 11 AAASO581/c ID AAASO581 standard; cDNA; 1514 BP.

9 CTTGTCAGGAGCGATAGGCTGC 30

Human; lymphocyte cell surface antigen; immune-mediated disease; CD28; infection; immune deficiency disorder; hypersensitivity; inflammation; systemic lupus erythematosus; platelet disorder; rheumatoid arthritis; transplant rejection; asthma; ss.

antigen"

"CD28

/*tag= a /product=

100. .153 /*tag= b 154. .759 /*tag= c

sig_peptide

mat_peptide

154. .75 /*tag=

Location/Qualifiers 100. .762

Homo sapiens.

Human lymphocyte cell surface antigen CD28 cDNA sequence.

(first entry)

29-AUG-2001

AAS03175;

AAS03175 standard; cDNA; 1514 BP.

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The present sequence encodes human CD28 receptor. CD28 is a homodimeric glycoprotein involved in a secondary signalling pathway in the activation of T-cell proliferation. B7 on nerve cells can interact with CD28 on the immune cell leading to immune cell activation. The regulation of cell surface expression of MHC classII and co-stimulatory molecule B7 can be manipulated by regulating the intracellular dissipation of proton motor force which can be assessed in terms of mitochondrial membrane potential. These methods can be used for regulating cell growth and division to control disease processes by manipulating mitochondrial metabolism and the expression of cell surface immune proteins. They can be used for treating diseases associated with excessive cellular division, aberrant differentiation, and premature cellular death, e.g. cancers, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                            Use of cell surface and membrane characteristics for developing products for treating cancers, autoimmune diseases or neurodegenerative diseases.
                                                                                                                      Human CD28; B7 molecule; immune response; cell surface receptor; Major histocompatibility complex; MHC classII; proton motor force; mitochondrial membrane potential; mitochondrial metabolism; cancer; autochommune disease; neurodegenezative disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases, neurodegenerative disorders etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 120-121; 123pp; English.
                                                                                                                                                                                                                   /*tag= a
/product= "Human CD28"
                                                                                                                                                                                             Location/Qualifiers
                                     AAZ29325 standard; cDNA; 1514 BP
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98US-0094519P.
98US-0101580P.
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/*tag= a
                                                                              (first entry)
                                                                                                    Human CD28 receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                       (UYVE-) UNIV VERMONT
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-096773/08.
                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY44294
                                                                                                                                                                                                                                                                                          30-MAR-1999;
                                                                               29-FEB-2000
                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                           Newell MK;
                                                           AAZ29325;
                             AAZ29325
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Simmons D;

Seed B, Aruffo A,

WPI; 2001-289848/30.

P-PSDB; AAU02437.

(GEHO) GEN HOSPITAL CORP.

89US-00379076.

92US-009B3647 88US-00160416

01-DEC-1992;

17-APR-2001

25-FEB-1988; 13-JUL-1989; 13-JUL-1990;

US6218525-B1

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The present sequence encoding for human lymphocyte cell surface antigen CD28 is used to obtain a new genetically engineered cDNA sequence encoding the CD28 amino acid extracellular domain sequence (amino acide in advortance) and on the comprising nucleotides 100-759, 154-555 or 134 given in AAU02437) and/or comprising nucleotides 100-759, 154-555 or 154-759 of the CD28 cDNA sequence. Various human lymphocyte cell surface antigen cDNA sequences (AAS03172, AAS03175, AAS03175, AAS03175, AAS03175, AAS03175, AAS03177, AAS03171, AAS03174) which provide high level expression vectors construction of cDNA libraries. Also described are 2 expression vectors (AAS03171, AAS03174) which provide high level expression in eukaryotic host cells. The purified genes and proteins are useful for immunodiagnostic and immunocherapeutic applications, such as in the disorders in animals and humans. Such diseases, infections or disorders and nimals and humans. Such diseases include immune deficiency diseases diseases of immediate type of hypersensitivity, asthma, hypersensitivity pneumonitis, systemic lupus erythematosus, rheumatoid other cell neoplasms, parasitic diseases, multiple sclerosis, Guillain-can also be used to identify, isolate and purify other antibodies and
New recombinant DNA encoding CD28 useful for diagnosing and treating immune-mediated diseases, infections or disorders, e.g. systemic lupus erythematosus, asthma, transplant rejection, rheumatoid arthritis.
                                                                                                                                                                                                                                              Example 3; Fig 7A-7B; 72pp; English.
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DB 4; Length 1514;

Score 20.4; I Pred. No. 37;

68.0%; 95.5%;

Query Match Best Local Similarity

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Gaps

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1; Indels

0; Mismatches

1 Similarity 95.5%; 21; Conservative

Best Local Similarity

Matches

Query Match

CGTGTCAGGAGCGATAGGCTGC 745 9 CTTGTCAGGAGCGATAGGCTGC 30

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RESULT 13 AAS03175/c

68.0%; Score 20.4; DB 3; Length 1514; 95.5%; Pred. No. 37;

Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;

complement fixation;

ds; Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CHZ constant region; High constant region; 1961; antibody dependent cell-mediated cytotoxicity; ADCC; complement fix: malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.

Unidentified.

Binding domain-immunoglobulin fusion protein-associated DNA #53

(first entry)

15-JAN-2004

ADD25537;

766 CGTGTCAGGAGCGATAGGCTGC 745

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BP

ADD25537 standard; DNA; 1514

ADD25537/c

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The sequence represents the human CD28 gene. The invention relates to a covel method for inhibiting an immune response by administering an anti-convel method for inhibiting an immune response by administering an anti-convel method of the invention has immunosuppressive, contiguoriatic, antidiabetic, antiarthritic, antirheumatic, neuroprotective, dermatological, vasotropic, antiloflammatory, contianaemic, hepatotropic, antiulcer, antibacterial and ophthalmological activity. The method works to inhibit immune by reversing or blocking T cell activation. The method is useful for inhibiting an immune response in a subject susceptible to graft-versus-host disease (GVHD), continuous and the continuous continuous arbitish and immune contransplant rejection, or paving autoimmune disease including psoriasis, clambetes mellitus, multiple sclerosis, rheumatoid arbitis, systemic clupus erythematosus, systemic sclerosis, dermatomycaitis, polymyositis, polymyositis, polymyositis, polymyositis, polymyositis, autoimmune heapsis, and other autoimmune diseases including autoimmune heapsis, and other autoimmune diseases including autoimmune heapsitis, autoimmune haemolytic anaemia, Behcet's disease, contrains gravis, cirrhosis, uncerative colitis, and vitiligo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease such as psoriasis, diabetes meilitus, multiple sclerosis, rheumatoid arthritis, polymyositis, by administering anti-CD28 antibody.
                                                                                                                                                                                                                                                                                                                                       Human; CD28; immune response; T cell; graft-versus-host disease; GVHD; marrow transplant rejection; organ transplant rejection; psoriasis; tissue transplant rejection; autoimmune disease; diabetes mellitus; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; systemic sclerosis; dermatomyositis; polymyositis; Sjogren's syndrome; polyarteritis nodosa; vasculitis; sepsis; gene; ds.
Gaps
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Indels
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95.5%; Pred. No. 37;
ive 0; Mismatches
Mismatches
                                                                              766 cerercaecaecearaecrec 745
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                                      30
                                          9 CTTGTCAGGAGCGATAGGCTGC
                                                                                                                                                                                   ABA99035 standard; DNA; 1514 BP
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                                                                                                                                                                                                                                                                 (first entry)
  21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YUXX/) YU X.
(ANAS/) ANASETTI C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu X, Anasetti C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002006403-A1.
                                                                                                                                                                                                                                                                                                          Human CD28 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-1999;
                                                                                                                                                                                                                                                                 13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 8
                                                                                                                                                                                                                           ABA99035;
    Matches
                                                                                                                                                                ABA99035
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                                                                                                                                                                                                                                                                                                                                                                            New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, gene, ss; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; hypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.4; DB 10; Length 1514; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                     Hayden-Ledbetter MS, Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 98; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI31990 standard; cDNA; 1514
                                                                                                                                                                                                                                                                     17-JAN-2001; 2001US-0367358P.
17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                                                                                                                                                                                                                  25-JUL-2002; 2002US-00207655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.0%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                                                                                                                                                                                                  (GENE-) GENECRAFT INC.
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-801317/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA #1316.
                                                                                                                                                                                                        US2003118592-A1.
                                                                                                                                                                                                                                                                                                                                       Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUN-2004
                                                                                                                                                                                                                             26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI31990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
ADI31990/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
à
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21; Conservative

Matches

Similarity

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Gaps

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surface antigen; immune-mediated disorder; asthma;
natoid arthritis; multiple sclerosis; vasculitis; inflammation; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cloning cDNA segments encoding cell surface antigens of human lymphocytes, useful in diagnosing and treating asthma, rheumatoid arthritis, multiple sclerosis, vasculitis and inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oquendo C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.4; DB 12; Length 1514; Pred. No. 37; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aruffo A, Camerini D, Lauffer L, kovic I, Stengelin S, Amiot M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    766 cererciaesaccariaecrec 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAN90607 standard; cDNA; 1574 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 7; 75pp; English.
                                                                                                                                                                                                                                                        89US-00379076.
90US-00498809.
90US-00553759.
92US-00983647.
                                                                                                                                                                                                  .7-APR-2001; 2001US-00836544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 68.0%;
Local Similarity 95.5%;
les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simmons D, Stamenkovic I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAMENKOVIC I.
STENGELIN S.
AMIOT M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-328571/30.
                                                                                                                                                                                                                                                                                                                                                                                                       CAMERINI D
                                                                                                                                                                                                                                                                                                                                                                                                                            LAUFFER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMMONS D.
                                                                                                                                                                                                                                                                                                                                                   SEED B.
ALLEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; ADO49344
                                                                                                                             US2004072283-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             OQUENDO
                                                                                                                                                                                                                                                                                                                                                                                       ARUFFO
                                                                                                                                                                                                                                                                                                                                                   SEED
                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2004
25-MAR-2003
31-OCT-2002
                                                                                                                                                                                                                                                                                                              01-DEC-1992;
                                                       gene; human.
                                                                                                                                                                                                                                         25-FEB-1988;
                                                                                                                                                                                                                                                                           23-MAR-1990;
                                                                                                                                                                                                                                                                                               .3-JUL-1990;
                                                                                                                                                                 15-APR-2004.
                                                                                                                                                                                                                                                          3-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections.
                                    rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN90607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SIMM/)
(STAM/)
(STEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seed B,
                                                                                                                                                                                                                                                                                                                                                   SEED/)
                                                                                                                                                                                                                                                                                                                                                                                                                                             OQUE/)
                                                                                                                                                                                                                                                                                                                                                                                                          CAME/
                                                                                                                                                                                                                                                                                                                                                                        ALLE/
                                                                                                                                                                                                                                                                                                                                                                                       ARUF/
                                                                                                                                                                                                                                                                                                                                                                                                                            LAUF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile compliant condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polymucleotide probes. The CDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polymucleotides. The microarray can be used in the diagnosis of an immunopathology, such as Crohn's disease, asthma, osteoarthitis, hyperresinophilia, irritable bowel syndrome, osteoarthitis, rheumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or comprising the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected hybridisation complexes with the level of hybridisation complexes
                                                                                                                                                                                                                                                                                                                             A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s patent did not form part of
in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%; Score 20.4; DB 11; Length 1514; 95.5%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1514 BP; 404 A; 360 C; 337 G; 413 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
osteopathic; antiarthritic; antirheumatic; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1316; 50pp; English.
                                                                                                                                                                                                                                                            Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            766 CGTGTCAGGAGCGATAGGCTGC 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO49343 standard; cDNA; 1514 BP
                                                                                                                                              98US-00023655
                                                                                                                                                                                   98US-00023655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 95.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CD28 antigen cDNA.
                                                                                                                                                                                                                                                          Stuart SG,
                                                                                                                                                                                                                     (INCY-) INCYTE CORP
                                                                                                                                                                                                                                                                                               WPI; 2003-895307/82.
                                                                                                                                                                                                                                                                                                                                                                                       or osteoarthritis.
                                    Homo sapiens
                                                                                                                                            09-FEB-1998;
                                                                                                                                                                                   09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2004
                                                                       US6607879-B1
                                                                                                           19-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from USPTO
                                                                                                                                                                                                                                                          Cocks BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADO49343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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ADO49343/
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Gaps

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8×4×4×8

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The sequence is an Xbal-Sall fragment encoding a chimeric receptor, composed of the extracellular region (XR) of leukocyte function-sesociated antigen-1 beta-chain (LFA-1-beta, of the integrin family), fused via the transmembrane region (TM) of CD28 to the integrin family), caused via the transmembrane region (TM) of CD28 to the interacellular region (IC28) of CD28. TM and IC28 coding sequences (bp 556-767) are amplified by PCR from human DD28 cDNA, and thex Rx coding sequences are cloned to form plasmid pSKLFA-1-beta/CD28, and subcloned in HyTK-CMV-Cat cloned to form plasmid pSKLFA-1-beta/CD28, and subcloned in HyTK-CMV-Cat into a psi-2 ecotropic packaging cell culture to give a stable PA317 cell into producing high titers of infectious particles, which are then used to infect T-lymphocytes. The resulting cytotoxic T-lymphocytes (CTLs) are selectively activatable, and have a lessened dependence on helper T-C lymphocytes (TH cells) and/or growth factors. The chimmeric receptor binds to the LFA-1 ligand (intercellular adheaion molecule-1, ICAM-1 or CD54) but IC28 transmits the proliferative signal of CD28. The CTB4 in directed cancer immunotherapy, and in treatment of viral infections
                                                                                                                                                                                                                                                                                                                                               i independent cytotoxic T lymphocytes useful in tumour or viral therapy are activated by adhesion to antigen displaying cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane region; intracellular domain; retrovirus; vector; packaging cell culture; gene transfer; ICAM-1; selective activation; cytotoxic T-lymphocyte; antitumour; immunotherapy; cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric receptor; LFA-1-alpha; extracellular domain; CD28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20.4; DB 2; Length 2405; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2405 BP; 503 A; 736 C; 739 G; 427 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 57-58; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2398 CGTGTCAGGAGCGATAGGCTGC 2377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFA-1-alpha-CD28 chimeric receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                   (TARG-) TARGETED GENETICS CORP.
                                                                                                                                                   94US-00332993.
95US-00480577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT27651 standard; cDNA; 3585
                                                                                                            95WO-US014171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.0%;
ilarity 95.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                           Feldhaus AL, Jones LA;
                                                                                                                                                                                                                                                                                                     WPI; 1996-239497/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 21; Conserv
                                                                                                                                                                                                                                                                                                                                          TH independent
                          WO9613584-A1.
                                                                                                            01-NOV-1995;
                                                                                                                                                      01-NOV-1994;
                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virucide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
                                                                  09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT27651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 20
      %XCCCCCCCCCCCCCX8X44X8XBXBXBXBXBXBXBXBX8X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is used for cloning into a vector which transforms COS cells. The vectors can be used to isolate any protein by immunoselection, and clones are easy to manipulate. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                               Tyrosine suppressor gene; ASV LTR; human cytomegalovirus AD169 enhancer; HIV box; immunoselection; immune deficiency diseases; vasculitis; systemic lupus erythematosus; rheumatoid arthritis; neoplasms; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chimeric receptor; LFA-1-beta; extracellular domain; CD28;
transmembranc region; intracellular domain; retrovirus; vector;
packaging cell culture; gene transfer; ICAM-1; selective activation;
cytotoxic T-lymphocyte; antitumour; immuncherapy; cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rapid immuno:selection cloning - used to clone genes encoding cell surface antigens associated with mammalian T lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lauffer L, Oquendo CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Revised record issued on 09-SEP-2004 : Correction to keywords
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%; Score 20.4; DB 1; Length 1574; 95.5%; Pred. No. 38; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1574 BP; 423 A; 375 C; 347 G; 429 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Camerini D,
                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFA-1-beta-CD28 chimeric receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 7; 69pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT27652 standard; cDNA; 2405 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                89EP-00103127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen J, Aruffo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88US-00160416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 95.5%;
les 21; Conservative
(first entry)
                                                                                                                                                                                                                                                       100. .819
/*tag= a
100. .274
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simmons D, Stamenkovi I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-250302/35.
                                       CD28 antigen cDNA.
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                                                                                                                                                                     Homo sapiens
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1988;
20-DEC-1989
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                                                                                                                                                                                                                                                                                                 sig peptide
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Key

Gaps

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Indels

WO9613584-A1

virucide; ss Homo sapiens

AAT27652/ ID AAT2 XX AC AAT2 XX AT2 XX BT2 DE LFA-XX Huma XW Huma XW Pack XW Cytco XX Viru

Matches

RESULT 19

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09-MAY-1996.

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29-AUG-2002
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202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                       The sequence is an XDaI-KpnI fragment encoding a chimeric receptor, composed of the extracellular region (XR) of leukocyte function-associated antigen-1 alpha-chain (LFA-1-alpha, of the integrin family), fused via the transmembrane region (TD28 to the intracellular region (IC28) of CD28. TM and IC28 coding sequences (bp 556-767) are amplified by PCR from human CD28 cDNA, and the XR coding sequence (bp 1-358) is amplified by PCR from human LFA-1-alpha (DD28. This retrovirus vector is cloned to form plasmid pSKLFA-1- alpha/CD28, This retrovirus vector is introduced into a psi-2 ecotropic packaging cell culture to give a stable PA317 cell line producing high titers of infectious particles, which are nused to infect T-lymphocytes. The resulting cytotoxic T-lymphocytes (CTLs) are selectively activatable, and have a lessened dependence on helper T-lymphocytes (TH cells) and/or growth factors. The chimeric receptor binds to the LFA-1 ligand (intercellular adhesion molecule-1, CTLs mediate lysis of a target cell bearing a cognate antigen, and are used to undered concer immunotherapy, and in treatment of viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; CD28; immune response; signaling; diabetes; autoimmune disease; immunosuppressive; dermatological; antiinflammatory; antithyroid; antirheumatic; antiarthritic; nootropic; allergy; rheumatoid arthritis; systemic lupus erythematosus; masthenia gravis; autoimmune thyroiditis; vitiligo; alopecia; inflammatory bowel disease; Addison's disease; draves disease; haemolytic anaemia; Sjogren's syndrome; gene; ds.
                                                                                                                                                                                                                                               TH independent cytotoxic T lymphocytes useful in tumour or viral therapy - are activated by adhesion to antigen displaying cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3585 BP; 808 A; 981 C; 1011 G; 785 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                      Example 1; Page 55-57; 82pp; English.
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/product= "CD28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL49546 standard; DNA; 3803 BP
                                                                                                             (TARG-) TARGETED GENETICS CORP.
                                        94US-00332993.
95US-00480577.
95WO-US014171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 68.0%;
Local Similarity 95.5%;
hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CD28 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                            Jones LA;
                                                                                                                                                                                                       WPI; 1996-239497/24.
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                                                                                                                                                       Feldhaus AL;
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                                          01-NOV-1994;
                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections
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XXX
AC AAL4
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DT 27-N
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The present invention relates to a method of therapeutically downmodulating an autoimmune response or an ongoing autoimmune response, comprishing administering an antigen binding portion of an anti-CD28 antibody that blocks signaling via CD28 to the subject so that an autoimmune response or an ongoing autoimmune response in the subject is downmodulated. The methods are useful in therapeutically and prophylactically downmodulating the immune response in subjects having autoimmune disorders such as diabetes, allergy and allergic reactions, transplantation rejection, graft versus host disease, systemic lupus erythematosus, rheumatoid arthritis, mysathenia gravis, autoimmune thyroiditis, vitiligo, alopecia, inflammatory bowel disease, Addison's disease, draves disease, haemolytic anaemia and Sjogren's syndrome. The present sequence is the human CD28 coding sequence
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lmmunostimulant; immunosuppressive; gene therapy; CD28; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                             Downmodulating immune responses by blocking CD28-mediated signaling, useful for preventing and/or treating autoimmune disorders such as diabetes, allergic reactions, graft versus host disease, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 3803 BP; 1076 A; 766 C; 880 G; 1081 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 60-61; 61pp; English.
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15-FEB-2002; 2002WO-US004772.
                                                                           16-FEB-2001; 2001US-0269756P.
                                                                                                                                                  (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2003 (first entry)
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                                                                                                                                                                                                                              O'hara RM, Nagelin AM;
                                                                                                                                                                                                                                                                                                         WPI; 2002-674899/72.
                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AA019101
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Claim 1; SEQ ID NO 1509; 245pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB72729;
                                                                                                                                                                                                                                                                                                             Query Match
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ADB72729/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                              to T-cell proliferation, or T-cell proliferation relative to T-cell survival. The method involves contacting a T-cell expressing a CD28 protein with an agent that selectively modulates the activity of a CD28 survival or proliferation motif relative to the activity of a CD28 proliferation motif respectively, to selectively modulate survival or proliferation of the T-cell. The method is useful in selectively modulating survival or proliferation of the T-cell. The method is useful in a subject. The method may also be used to prevent or treat disorders associated with associated disorders, allergic diseases, transplant-associated disorders, allergic diseases, graft-versus-host disease, lymphoproliferative disorders or autoimmune diseases. The present sequence represents a DNA encoding the human CD28 protein
                                                                                                                                                                       invention relates to selectively modulating T-cell survival relative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, carcinoma associated, oncogene, carcinoma, cancer, breast, prostate, lymphoma, leukaemia, cytostatic, gene therapy, drug screening,
                                                                                        Selectively modulating T-cell survival or proliferation, useful for treating autoimmune diseases, comprises contacting T-cells expressing DD8 protein with agents that modulate activity of CD28 survival or proliferation motif.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                         Score 20.4; DB 8; Length 3804; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                   Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CD28 carcinoma associated cDNA, SEQ ID NO:1509.
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                               Disclosure, Page 115-117; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    889 CGIGICAGGAGCGAIAGGCIGC 868
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                                                                                                                                                                                                                                                                                                                                                        68.0%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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           (UNIW ) UNIV WASHINGTON
                                                       WPI; 2003-111968/10.
P-PSDB; ABB82721.
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                                 Shaw AS;
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                 Green JM,
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                                                                                                                                                                                                                                                                                                                                                         Query Match
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to crecombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a cinvention also encompasses expression vectors and host cells comprising a comprising to the protein, and a blochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retrovirues, which insert into the genome of the host organism or a random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or carcinoma (especially breast cancer, prostate cancer, lymphoma or carcinoma (especially breast cancer, prostate cancer, lymphoma or tissues. CA nucleic acids, proteins and antibodies are also useful as therespettic agents and in screening and expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as thereapeutic agents and in screening and evaluating drug candidates. The present sequence of the printion. Note: The complete sequence data for this cancer in electronic format didectly from WIPO at an electronic format didectly from WIPO at electronic format didectly from WIPO at electronic format didectly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 557; 2304pp; English
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23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-239337/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003008583-A2
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Gaps

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Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA; secreted; transmembrane; intracellular; ds.
                           The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynuclectide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
                                                                                                                                                                                                                                                           sarcomas. The present sequence represents a human mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant nucleic acid comprising a nucleotide sequence of any of
the carcinoma-associated (CA) genes, useful for screening for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nuclectide sequence selected from any of the fully defined carcinoma-
associated (CA) genes from the 50 tables given in the specification. The
CA proteins are secreted, transmembrane or intracellular proteins. The
recombinant nucleic acids are useful for screening for drug candidates
for diagnosing or treating carcinomas. Sequences given in ADC85215-
ADC85514 represent CA genes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 3804;
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                                                                                                                                                                                                                                                                                                                                 Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.4; I
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         889 CGTGTCAGGAGCGATAGGCTGC 868
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                                                                                                                                                                                                                                                                                                                                                                                                               68.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Cd28 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-513603/48.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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ADC85471/
ID ADC85471/
ADC85471/
ADC871/
ADC
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The invention relates to new recombinant nucleic acids. The invention also relates to a host cell comprising a recombinant nucleic acid of also relates to a host cell comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, a method of screening for a bioactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma drug, a method of diagnosing carcinoma, a method of inhibiting carcinoma drug, a method of diagnosing carcinoma, a method of diagnosing carcinoma, a method of carcinoma and comprises administering the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of consor more genes comprising the nucleic acid sequence in a first tissue trype for a first individual and comparing the expression of the gene from a second normal tissue type from the first individual or a second normal tissue type from the first individual or a second carcinomas comprises diading an inhibitor to the CAP. Treating carcinomas comprises administering to a patient an inhibitor of CAP. Neutralising the effect of a CAP comprises contacting an agent specific for the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. The nucleic acid of the invention. Note: The sequence corpusions or lymphoma. This sequence represents a human carcinoma corpusions or lymphoma. This sequence represents a busing captained in electronic format directly from USPTO at
                                                                                                                                                                                 Human, carcinoma associated nucleic acid; CA nucleic acid; gene; st
carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                                                                                                                         Human carcinoma associated (CA) nucleic acid #128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 257; 29pp; English.
                 ADM74586 standard; DNA; 3804 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2000; 2000US-00747377.
02-MAR-2001; 2001US-00798586.
                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-2001; 2001US-00997722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MORR/) MORRIS D W. (ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-328562/30.
                                                                                                                                                                                                                                                                                                               US2004072154-A1.
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                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       15-APR-2004.
                                                                                                  01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morris DW,
                                                                                                                                                                                                                                 cytostatic.
                                                           ADM74586;
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ADM74586/
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Query Match 68.0%; Score 20.4; DB 10; Length 3804; Best Local Similarity 95.5%; Pred. No. 43; Matches 21; Conservative 0; Mismatches 1; Indels 0;

889 CGTGTCAGGACGATAGGCTGC 868

CTTGTCAGGAGCGATAGGCTGC 30

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2002-017603/02.
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                                                                                                                         WO200179300-A1.
                                                                                                                                                                                                               Bluestone JA,
                                                             Homo sapiens
                                                                                                                                                                                                                                                                                     molecule
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ID ADA00
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                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                             Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in
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                Score 20.4; DB 12; Length 3804;
Pred. No. 43;
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Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3804 BP; 1076 A; 766 C; 880 G; 1082 T; 0 U; 0 Other;
                                                                                                                                                                                      ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                  1;
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                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2250; 3069pp; English.
                                                               CGTGTCAGGAGCGATAGGCTGC 868
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                                                   9 CTTGTCAGGAGCGATAGGCTGC 30
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                                                                                                                                                                    Antipsoriatic cDNA sequence #1159
                                                                                                                ADN05855 standard; cDNA; 3804 BP
                                                                                                                                                                                                                                                                            25-SEP-2002; 2002US-0414006P.
                  68.0%;
95.5%;
                                                                                                                                                                                                                                                          25-SEP-2003; 2003WO-US030907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD21976 standard; DNA; 3806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.5%;
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        Query Match
Best Local Similarity 95.5.
Best Local 21, Conservative
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                        WPI; 2004-305105/28.
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                                                                                                                                                                                                                       WO2004028479-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CD28 DNA
                                                                                                                                                   01-JUL-2004
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                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                 ADN05855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                             RESULT 28
AAD21976/
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The invention relates to a construct for downmodulating immune response in a subject. The construct comprises an exposed surface attached with an attigen-binding portion of an antibody that binds to a cytotoxic T lymphocytic antigen (CTLA) -4 or CD28 expressed on T-cell of the subject, and a major histocompatibility complex (MHC) molecule. The construct is useful for treating an individual afflicted with a disease or disorder that would benefit from downregulation of immune response. Downmodulation of the immune response is useful to downmodulate the immune response in autorimmune diseases such as systemic lupus erythematosus and multiple sclerosis. The construct is useful for inhibiting immune cell activation and prevents production of autoantibodies or cytokines which may be involved in disease production of immune cell activation is useful in the treatment of allergy and allergic reactions of the construct is also useful in viral immunity or in immunodeficiency diseases cuch as AIDS and DiGeorge Syndrome. Induction/enhancement of immune cell function results in increased tumour destruction in cancer patients. The construct is also useful in treating infectious diseases. The present sequence is human CD28 DNA
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Human, cytotoxic T lymphocyte antigen-4; CTLA-4; CD28; AIDS; therapy; Acquired Immune Deficiency Syndrome; neuroprotective; dermatological; immune response; organ transplantation; autoimmune disease; allergy; SLE; systemic lupus erythematosus; multiple sclerosis; tumour vaccination; immunodeficiency disease; DiGeorge Syndrome; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New construct for downmodulating immune response in a subject, has exposed surface attached with antigen-binding portion of antibody that binds to cytotoxic I lymphocyte antigen-4 and major histocompatibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffin M, Kranz D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Human CD28 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Matches 21; Conservative
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03994), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a invention also encompasses expression vectors and host cells comprising a carcinoma also encompasses expression vectors and host cells comprising a carcinoma blocker. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism car random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protoconcogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or a propensity to carcinoma by determination of the sequence carcinoma (especially breast cancer, prostate cancer, lymphoma or tissues. CA nucleic acids, proteins and antibodies are also useful as therement sequence represents a specifically claimed human CA nucleic acid format did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
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                                                                                                        Human, carcinoma associated, oncogene, carcinoma, cancer, breast;
prostate, lymphoma, leukaemia, cytostatic, gene therapy; drug screening,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
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                                                                     Human CD28 carcinoma associated gene, SEQ ID NO:1508.
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Les 21, Conservative
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                                                                                                                                                                                     Homo sapiens.
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 ADA02990;
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ADB72728/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
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                        human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
cancer; neoplasm; adenocarcinoma; sarcoma; gene.
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23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00957482.
30-NOV-2001; 2001US-00934650.
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                                                                                                                                                    26-DEC-2001; 2001WO-US051291.
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                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY
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Human CD28 gene.
                                                                                             WO2003008583-A2.
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                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                        The
                                                                                                                                                       New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug
                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The A proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51365 BP; 15176 A; 10059 C; 10474 G; 15656 T; 0 U; 0 Other;
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                                                                                                                                                                                                                              candidates for diagnosing or treating carcinomas.
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                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 256; 983pp; English.
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                                 Engelhard EK;
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                                                                                              WPI; 2003-513603/48.
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hes 21; Conserv
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                                 Morris DW,
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ID ADM74588
AC ADM7488
XX ADM7488
XX Human, CXX Human, CXX Carcinc
XX Human, XX Carcinc
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method of screening for a bloative agent capable of modulating the activity of a CAP, a method of evaluating the effect of a candidate carcinoma drug, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method of the activity of a CAP, a method of treating carcinoma, a method of the activity of a CAP, a method of treating carcinoma, a method of the activity of a CAP, a method of treating carcinoma, a method of carcinoma drug comprises administering the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a cell sample from the patient and determining alterations in the expression or activation of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of the gene comprising the nucleic acid sequence in a first tissue type from the first individual and comparing the expression of the gene from a second normal tissue type from the first individual or a second activity of a CAP comprises binding an inhibitor to the CAP. Treating carcinoma a method of inhibiting the carcinomas comprises administering to a patient an inhibitor of CAP. Observable of the invention and a composition for diagnosing or treating carcinoma e.g., the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acids are useful for protein encoded by the nucleic acid. The nucleic acids are useful for protein encoded by the nucleic acid of the invention. Note: The sequence data associated (CA) nucleic acid of the invention. Note: The sequence data composition format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCR; CD3 zeta chain; co-stimulatory signalling region; immunostimulant; therapy; cancer; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid polymer encoding a chimeric T cell receptor having a zeta chain portion, useful for treating disorders where the immune response needs to be induced, such as cancer.
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carcinoma associated protein (CAP) encoded by a nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51365 BP; 15176 A; 10059 C; 10474 G; 15656 T; 0 U; 0 Other;
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95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T cell receptor;
binding element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004043401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sadelain M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL67233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell
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Matches
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ADL67233
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Query Match
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                       The invention relates to a nucleic acid polymer encoding a chimeric T cell receptor (TCR) which comprises human CD3 zeta chain intracellular domain, a co-stimulatory signalling region and a binding element that specifically interacts with a selected target. The methods and compositions of the invention are useful for treating disorders where the imamue response needs to be induced, such as cancer. The present sequence is a PCR primer used to amplify human CD28 costimulatory molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel tumor-associated antigen recognized by murine monoclonal antibody 8H9, expressed on cell membranes of broad spectrum of tumors, useful for producing antibodies capable of inhibiting tumor cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a protein (I), in particular tumourassociated antigen 58 kilo Daltons (kDa) in molecular weight, reacting specifically with monoclonal antibody (MAD) 8H9 Also described: (1) a composition (C) comprising MAD 8H9 or its derivative; (2) an antibody produced by immunising (I) or its specific portion; and (3) an antibody (II) produced by using (I). (I) has antitumour activity and can be used in antibody-based therapy. (I) can be used for producing a MAD, and to evaluate the tumour bearing potential of a subject, by measuring the expression of 8H9 antigen in the subject, where an increased expression of the antigen indicates higher tumour bearing potential of the subject. (II) or (C) comprising 8H9 or its derivative are useful for inhibiting the growth of tumour cells in vitro or in vivo, and the antibody indirectly coupled to a cytotoxic agent (radioisotope) is useful for
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody 8H9; tumour-associated antigen; 8H9 antigen; immunisation; antitumour; antibody-based therapy; tumour; cytotoxic; tumour bearing potential; cancer; Ewing's sarcoma; primer; ss.
                                                                                                                                                                                                ö
                                                                                                                                                                      DB 12; Length 36;
                                                                                                                                                                                              3; Indels
                                                                                                                                            Sequence 36 BP; 7 A; 9 C; 14 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                     Score 20.2; I
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SLOK ) SLOAN KETTERING INST CANCER RES
 Example 1; SEQ ID NO 8; 25pp; English.
                                                                                                                                                                                                                        6 GATCTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                          2 GCTCGAGTCAGGAGCGATAGGCTGC 26
                                                                                                                                                                                                                                                                                                                                                                                                Human CD28 355 A antisense primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 142; 209pp; English.
                                                                                                                                                                                                                                                                                                                  ABN88948 standard; DNA; 31 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001; 2001WO-US032565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000; 2000US-0241344P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0330396P
                                                                                                                                                                      67.3%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                              22; Conservative
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                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200232375-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                      22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                            ABN88948;
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                Matches
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incorporating an Xhol restriction site. It was used with primer 3555 sense primer (see ACF80095) in the PCR amplification of an hCD8a leader-849 scFV-CD8 construct. The construct was used in a series of experiments in which an anti-idiotype antibody was used to enhance ScFV chimeric immune receptor gene transduction and clonal expansion of human lymphocytes. The invention provides a composition comprising 8H9 or its derivative, such as an scFV or ScFV-FC, and a suitable carrier. The antibody may comprise the CDRs of 8H9 with its remaining sequence being human. Also claimed are nucleic acids encoding the antibodies, vectors, cells comprising the vectors, and methods of producing the antibodies. The method for directly killing or delivering a drug, DNA or RNA to cells bearing the antigen using an 8H9 ScFV or a 8H9-ScFV-modified cell or inhibiting the growth of tumour of the antipod of tumour bearing potential of a subject, or (when coupled to a cytotoxic agent) reducing tumour cells, imaging a tumour, evaluating the cumour cells in the subject, or (when coupled to a cytotoxic agent) reducing tumour cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising the monoclonal antibody 8H9 useful for reducing tumor cells in a subject, evaluating the tumor bearing potential of a subject or screening new anti-tumor compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody; 8H9; antitumour; cytostatic; gene therapy; human;
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of 355A antisense primer for human CD28,
reducing tumour cells in a subject. The present sequence represents a primer which is used in the exemplification of the present invention
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                                                                                                                                                                             66.7%; Score 20; DB 6; Length 31; 100.0%; Pred. No. 32;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31 BP; 5 A; 6 C; 12 G; 7 T; 0 U; 1 Other;
                                                                                                         Sequence 31 BP; 5 A; 6 C; 12 G; 7 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CD8a leader 355A antisense PCR primer.
                                                                                                                                                                                                       100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SLOK ) SLOAN KETTERING INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 124; 190pp; English.
                                                                                                                                                                                                                                                                                                                       11 TGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                               12 TGTCAGGAGCGATAGGCTGC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAR-2003; 2003WO-US007004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2002; 2002US-00097558.
17-OCT-2002; 2002US-00273762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2002; 2002WO-US03331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACF80096 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD28; PCR; primer; ss.
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                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003075846-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheung NV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACF80096;
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                  Matches
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DB 10; Length 31;

66.7%; Score 20;

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Primer P3241 was used with primer P3240 (see AAT90525) in the PCR cloning of the human CD28 transmembrane and intracellular components using human leukocyte cDNA as template. P3241 introduces a 3' EcoRI site and P3240 introduces a 5' BamHI site. The PCR product was subcloned into pBluescript SK+ to form a CD28 cassette. Primer P3241 was also used with primer S0146 (see AAT90533) to produce a hinge-CD28 cassette. These cassettes can be utilised in novel chimeric genes (see AAT90510-11 and AAT90513-14) encoding recombinant chimeric receptors (see AAM2647-48 and AAW36650-51) useful in cell activation processes, e.g. for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell activation; chimeric receptor; DNA delivery; CD28; T cell receptor; human; cancer; therapy; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                        New DNA systems for activating cells - comprising DNA coding for a chimeric receptor comprising 2 or more different cytoplasmic signalling
     Cell activation; chimeric receptor; DNA delivery; CD28; human; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T cell receptor zeta chain-CD28 fusion cassette primer P3303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30 BP; 9 A; 5 C; 9 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         Finney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.4; DE
Pred. No. 60;
0; Mismatches
                                                                                                                                                                                                                                                                           Weir ANC,
                                                                                                                                                                                                                                          (CLLT ) CELLTECH THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Trcrcaggagcgaraggcrgc 27
                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 3; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 TTGTCAGGAGGGATAGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                       96WO-GB003209
                                                                                                                                                                                                         95GB-00026131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                           Lawson ADG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT90529 standard; DNA; 64
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                      therapy; PCR; primer; ss
                                                                                                                                                                                                                                                                                                         WPI; 1997-351052/32.
                                                                                                                                                                                                                                                                           Bebbington CR,
                                                                       Homo sapiens.
                                                                                                                                                                       23-DEC-1996;
                                                                                                     WO9723613-A2
                                                                                                                                                                                                         21-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1995;
                                                                                                                                      03-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                             components.
                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT90529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a method of making a single chain antibody (scFv) directed against an antigen, where the selection of clones is made based upon interaction of those clones with an appropriate anti-idiotype. The method is useful for making a single chain antibody directed against an antigen. PCR primers ACC70421.22 were used to construct a chimeric immune receptor, comprising the human CD8a leader, a scFv and CD28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing single chain antibody directed against an antigen, by selecting clones using anti-idiotype antibody directed to antibody specific for the
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                       Single chain antibody; scFv; antigen; CD8a; CD28; PCR; primer; ss.
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Pred. No. 32;
                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31 BP; 5 A; 6 C; 12 G; 7 T; 0 U; 1 Other;
     Pred. No. 32;
Best Local Similarity 100.0%; Pred. No. 32; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prea. ... 0; Mismatches
                                                                                                                                                                                                                                                                        used to amplify human CD28 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SLOK ) SLOAN KETTERING INST CANCER RES.
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                                                                            TGTCAGGAGCGATAGGCTGC 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCAGGAGCGATAGGCTGC 30
                                                    TGTCAGGAGCGATAGGCTGC 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2001; 2001US-0330396P.
18-OCT-2001; 2001WO-US032565.
08-MAR-2002; 2002US-00097558.
                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2002; 2002WO-US03331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
                                                                                                                                                                       ACC70422 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-393522/37
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Matches 20, Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guo H;
                                                                                                                                                                                                                                                                                                                                                                          WO2003033670-A2
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                                                                                                                                                                                                                                      11-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2003.
                                                                                                                                                                                                                                                                         primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheung NV,
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                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                    7
                                                                                                                                                                                                     ACC70422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
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AAT90526
ID AAT90
XX
AC AAT90
XX
XX
DT 12-FE
XX
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Gaps

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Indels

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Plant; bacterial infection; fungal infection; viral infection; rice;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64 BP; 16 A; 25 C; 10 G; 13 T; 0 U; 0 Other;
                            Finney HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19.4; DE Pred. No. 67; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              processes, e.g. for the treatment of cancer
                            Weir ANC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 rrcrcagaaccaraccrcc 38
                                                                                                                                                                                                                                              Example 1; Fig 3; 90pp; English.
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                            Lawson ADG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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                                                                                  WPI; 1997-351052/32
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                            Bebbington CR,
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AC ADA694
AC ADA69
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.

WO200175067-A2

11-OCT-2001.

Homo sapiens

DNA encoding novel human diagnostic protein #17370.

(first entry)

13-FEB-2002

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Gaps

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BP

The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) or to treat disease states involving (II). (II) is activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The colypeptide and polymucleotide sequences have applications in diagnostics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess Claim 1; SEQ ID NO 17370; 103pp; English. 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang YT WPI; 2001-639362/73. Drmanac RT, Liu C, (HYSE-) HYSEQ INC. P-PSDB; ABG17379 biodiversity. t 2 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 ö

Hou Y; T, Zou

Glazebrook J, Goff SA, Ho Whitham S, Xie Z, Zhu T,

'n ≯

Cooper S, Tao

Katagiri F, Quan S, WPI; 2003-175290/17.

Chen W,

r

Chang

Claim 6; SEQ ID NO 2739; 899pp; English

gene expression

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comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                       Sequence 852 BP; 219 A; 230 C; 267 G; 136 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 ccaddarcrcrcaddadccadaadcrdc 445
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                                                                                                                                                                                                                                                                  illustrate the invention.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 Primers P3301, P3302, P3303, P3304, P3305 and P3306 (see AAT90527-32) were used for the PCR assembly of a human T cell receptor zeta-CD28 fusion cassette. The 3' end of zeta, starting at the native Styl site, and the intracellular component of human CD28 were PCR assembled such that the zeta stop codon was removed and an in-frame fusion protein would be translated. The PCR product was subcloned into pBluescript SK+ containing a CTMO1 TCR zeta chimeric receptor construct, replacing the 3' end of zeta. The zeta-CD28 fusion cassette can be utilised in novel chimeric genes (see AAT90510 and AAT90513) encoding recombinant chimeric receptors (see AAW26647 and AAW26650) useful in cell activation
                                                                                                                                                                                 New DNA systems for activating cells - comprising DNA coding for a chimeric receptor comprising 2 or more different cytoplasmic signalling
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Gaps

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Indels

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0; Mismatches

8; Length 852;

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Score 19.4; Pred. No. 98

64.7**%**; 79.3**%**;

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cc and to produce other types of data and products dependent on DNA and conding sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this cc patent did not appear in the printed specification, but was obtained in cc electronic format directly from WIPO at cc ftp.wipo.int/pub/published_pct_sequences

XX

Query Match

G4.7%; Score 19.4; DB 5; Length 1156;

Best Local Similarity 79.3%; Pred. No. 1e+02;

Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Search completed: January 7, 2005, 11:40:49 Job time: 230.421 secs

1 TCGAGGATCTTGTCAGGAGGGATAGGCTG 29

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Query Match
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Sequence 1316, Appl
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                                                                                                                                                                                                                                                 January 7, 2005, 10:58:39; Search time 54.2105 Seconds (without alignments) 393.349 Million cell updates/sec
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/cgm2_6/ptodata/1/ina/6A_COWB.seq:*
/cgm2_6/ptodata/1/ina/6B_COWB.seq:*
/cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-529-846-2

US-08-529-846-7

US-09-716-129-46

US-09-716-129-6

US-09-774-528-129

US-09-270-767-16309

US-09-270-767-1437

US-09-252-991A-7065

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US-09-270-767-19421

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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GENERAL INFORMATION:

APPLICANT: FELDHAUS, ANDREW L.

APPLICANT: PELDHAUS, LORI A.

TITLE OF INVENTION: CHIMMERIC RECEPTORS FOR THE GENERATION OF

TITLE OF INVENTION: SELECTIVITY-ACTIVATABLE T(h)-INDEPENDENT CYTOTOXIC T CELLS

TITLE OF INVENTION: SELECTIVITY-ACTIVATABLE T(h)-INDEPENDENT CYTOTOXIC T CELLS

TITLE OF INVENTION: SELECTIVITY-ACTIVATABLE T(h)-INDEPENDENT CYTOTOXIC T CELLS

TORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & POERSTER

STRET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA
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Sequence 33
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,846
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER:
REGISTRATION NUMBER: 22627-20013.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION
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                                                                                          US-09-601-040A-11

US-07-882-925A-4

US-08-184-012C-4

US-08-184-012C-4

US-07-882-925A-1

US-07-882-925A-1

US-08-184-012C-1

US-08-134-177-1

US-08-134-177-1

US-08-134-177-1

US-08-134-177-1

US-08-134-177-1

US-08-131-336-1

US-08-131-336-1

US-08-620-112D-337

US-08-131-337-1

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ZIP: 94304-1018
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CTTGTCAGGAGCGATAGGCTGC 30
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Patent No. 6083751
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Matches 21; Conservative
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US-08-549-846-1/c
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Sequence 3, Application US/08549846
Patent No. 6083751
CENERAL INFORMATION:
APPLICANT: FELDHAUS, ANDREW L.
APPLICANT: JONES, LORI A.
TITLE OF INVENTION: SELECTIVITY-ACTIVATABLE T(h)-INDEPENDENT CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.0%; Score 20.4; DB 4; Length 1514; Best Local Similarity 95.5%; Pred. No. 2.9; Matches 21; Conservative 0; Mismatches 1; Indels 0.
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compariable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION NATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1316:
TENERAL 1514 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Riopy disk
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
SOCTAME: Patentin Release #1.0, Version #1.30
SOCTAME: Patentin Navle: US/08/549,846
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: US/08/549,846
FILING DATE: 01-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DYLAM, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
TELEPHONIC: (415) 813-5600
TELEPHON: (415) 813-5600
TELEPHON: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1514 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CLONE: 9338444
US-09-023-655-1316
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US-09-023-655-1316/c
; Sequence 1316, Application US/09023655
; Patent No. 6670879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
; APPLICANT: Office G. Stuart
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; WUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

68.0%; Score 20.4; DB 2; Length 1064;
Best Local Similarity 95.5%; Pred. No. 2.7;
Matches 21; Conservative 0; Mismatches 1; Indels 0
                                                                  Sequence 40, Application US/08529878B
Patent No. 5932556
GENERAL INPORMATION:
APPLICAMT Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish STREET: 3000 S. Augusta Court CITY: La Habra STARET: al Abbra COUNTRY: United States of America STARET: United States of America STARE: United States of America STARE: United States of America STARE: HEM PC Compatible OWNFUTER READBALE FORM: MEDIUM TYPE: PLOPDY disk COMPUTER: HEM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Fish, Robert D: REGISTRATION NUMBER: 33,880
REGISTRATION NUMBER: 33,880
REGISTRATION NUMBER: 213/003
TELECPMA: 714-525-3433
TELECPMA: 714-525-3433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 CGTGTCAGGAGCGATAGGCTGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 1..309
US-08-529-878B-40
                            RESULT 2
US-08-529-878B-40/c
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COUNTRY: US
ZIP: 94304
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DB 2; Length 20;
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                                   APPLICANT: Tam, Robert C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Crockett & Fish
STREET: 3000 S. Augusta Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL LINCARIALION:
J GENERAL LINCARIALION:
J TITLE OF INVENTION: 36 Human Secreted Proteins
FILE REFERENCE: P2025F1
CURRENT APPLICATION NUMBER: US/09/716,129
CURRENT FILING DATE: 2000-11-17
PRIOR PILING DATE: 1938-02-26
PRIOR FILING DATE: 1938-02-26
PRIOR PRICH DATE: 1938-02-26
PRIOR PRICH DATE: 1938-02-26
PRIOR FILING DATE: 1938-02-26
PRIOR PILING DATE: 1938-02-26
PRIOR PRICH DATE: 
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                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/529,878B
FILING DATE: 13-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fish, ROBERT D.
REGISTRATION NUMBER: 33,880
                                                                                                                                                                                                                                                                                                              STATE: California
COUNTRY: United States of America
ZIP: 90631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/09716129
Patent No. 6632920
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-525-3433
TELEFAX: 714-525-3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-18
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs:
TYPE: nucleic acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                           CITY: La Habra
STATE: Californ
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Sequence 2, Application US/08549846
Batent No. 608371
GENERAL INFORMATION:
APPLICANT: FELDHAUS, ANDREW L.
APPLICANT: JONES, LORI A.
TITLE OF INVENTION: CHIMERIC RECEPTORS FOR THE GENERATION OF
TITLE OF INVENTION: SELECTIVITY-ACTIVATABLE T(h)-INDEPENDENT CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                           Query Match 68.0%; Score 20.4; DB 3; Length 2405; Best Local Similarity 95.5%; Pred. No. 3.2; Matches 21; Conservative 0; Mismatches 1; Indels 0
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Pred. No. 3.6;
0; Mismatches 1; Indels 0
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COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPA:

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/549,846

FILING DATE: 01-NOV-1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFRENCE/DOCKET NUMBER: 22627-20013.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEFAX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3578 cerercacaccaracerec 3557
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; Sequence 18, Application US/08529878B
; Patent No. 5932556
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGTCAGGAGCGATAGGCTGC 30
TELEX: 706141 MRSNFOERS SFO
| INFORMATION FOR SEQ ID NO: 3:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 2405 base pairs
| TYPE: nucleic acid
| STRANBEDNESS: single
| TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.0%;
Best Local Similarity 95.5%;
Matches 21; Conservative (
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US-08-549-846-2/c
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0; Gaps

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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1027
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Best Local Similarity 80.8%;
Matches 21; Conservative
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Best Local Similarity 100.'
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 bases
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11:
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                                                                            Gaps
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| Batent No. 6221637
| GENERAL INFORMATION
| TITLE OF INVENTION: XANTHENE DERIVATIVES, THEIR PRODUCTION AND
| TITLE OF INVENTION: USE
| NUMBER OF SEQUENCES: 11
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Wenderoth, Lind & Ponack
| STREET: 805 Fifteenth Street, N.W., #700
| STATE: D.C.
| COUNTRY: U.S.A.
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                                  63.3%; Score 19; DB 4; Length 1189;
81.5%; Pred. No. 13;
ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 4; Length 4758; Pred. No. 18; 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743519el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                               361 GAGGATTTTGCCAGGTGGGATGGGCTG 335
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                                                                                                          3 GAGGATCTTGTCAGGAGCGATAGGCTG 29
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CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: DL_FL_Genes Version 2.0
                                                                                                                                                                                                                                     Sequence 129, Application US/09774528
Patent No. 6743619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.3%;
Best Local Similarity 81.5%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                              Liu, chenghua
Asundi, Vinod
Ren, Peiyan
Zhao, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Dunrui
                                  Query Match 63.3
Best Local Similarity 81.5
Matches 22; Conservative
                                                                                                                                                                                                                                                                                        Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (167)..(4381)
US-09-774-528-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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US-09-716-129-46
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US-08-812-946A-7
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APPLICANT Homburger et al.
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-034
CURRENT PELLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1027
LENGTH: 268
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US-002-270-767-16309
US-002-270-767-16309
Sequence 16309, Application US/09270767
Fatent No. 6703491
Fatent No. 6703491
FAPPLICANT: Homburger et al.
FILE REPREMENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
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Pred. No. 26;
0; Mismatches 5; Indels
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other nucleic acid, Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
CURRENT APPLICATION DATA:
SOFTWARE:
Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,946A
FILING DATE: March 4, 1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, UF.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECHOUNICATION INFORMATION:
TELECHOUNICATION INFORMATION:
TELECHOUNICATION INFORMATION:
TELECHOUNICATION INFORMATION:
TELECHOUNICATION INFORMATION:
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US-09-181-339-4
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Patent No. 6703491
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17497
LENGTH: 746
                                                                                                                                                                                                                                                                                                                                                                               Sequence 2215, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2215
LENGTH: 746
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                                                                                                                                                                                                       5; Indels
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; ORGANISM: Drosophila melanogaster
US-09-270-767-17497
                                                                               ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-09-270-767-2215
                                                                                                                                                           Query Match
Best Local Similarity 80.8%;
Matches 21; Conservative
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16309
LENGTH: 268
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Best Local Similarity 80.0
Local Similarity 80.0
Local Similarity 80.0
Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-270-767-2215
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RESULT 14 US-09-270-767-15260/c

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; Sequence 15260, Application US/09270767; Patent No. 6703491.; Patent No. 6703491.; GENERAL INPORMATION:
; APPLICANT: Homburger et al.; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; CURRENT APPLICATION UNDER: US/09/270,767
; CURRENT APPLICATION UNDER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 15260
LENTH: 1498
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15260
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Fatent No. 6610827
GENERAL INFORMATION:
APPLICANT: Porsayeth, John R.
APPLICANT: Chavez, Raymond C.
TITLE OF INVENTION: POLYNUCLECTIDE COMPOSITIONS AND USES THEREFOR TITLE OF INVENTION: POLYNUCLECTIDE COMPOSITIONS AND USES THEREFOR FILE REFERENCE: 5865-0033.30
CURRENT PILING DATE: 1998-10-28
FRIOR APPLICATION NUMBER: US 60/063,450
PRIOR FILING DATE: 1997-10-29
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US-09-221-017B-726/c
; Sequence 726, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; ATILE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 18; DB 4; Length 1498; Best Local Similarity 80.8%; Pred. No. 40; Matches 21; Conservative 0; Mismatches 5; Indels
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Best Local Similarity 75.9%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  502 GGATCTTGTGACGATCGATTGGCGGC 477
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: (2)...(772)
US-09-181-339-4
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US-09-252-991A-7120/c

is Sequence 7120, Application US/09252991A

is TITLE OF INVENTION: NUCLEIC ACID ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS

is TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

is TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

is FILE REFREENCE: 107196-136

is PRIOR APPLICATION NUMBER: US 60/074,788

is PRIOR APPLICATION NUMBER: US 60/094,190

is PRIOR PILING DATE: 1998-02-18

is PRIOR PILING DATE: 1998-07-27

is NUMBER FOR SEQ ID NOS: 33142

is SEQ ID NO 7120

LENGTH: 3186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERBNCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SEQ ID NO 7009
LENGTH: 2910
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                                                                                                                                                                                                 Gaps
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                                                                                                                                     Query Match 58.0%; Score 17.4; DB 4; Length 1758; Best Local Similarity 77.8%; Pred. No. 81; Matches 21; Conservative 0; Mismatches 6; Indels 0
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                                                                                                                                                                                                                                                         3 GAGGATCTTGTCAGGAGCGATAGGCTG 29
                                                                                                                                                                                                                                                                                                            125 GAGGATCCCGTCATGACCGATAACCTG 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7009, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                          ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7065
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CORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7120
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US-09-252-991A-7009
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LENGTH: 1758
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Sequence 7065, Application US/09252991A
Sequence 7065, Application US/09252991A
Sequence 7065, Application US/09252991A
Sequence 7065, Application US/09252991A
Sequence 7065, Application
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 10196.02-18
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.3%; Score 17.8; DB 4; Length 1974; Best Local Similarity 75.9%; Pred. No. 54; Matches 22; Conservative 0; Mismatches 7; Indela n
                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               983 rcegesekerrerceczasaka pss
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                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
PRING APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PP2911
FILING DATE: 00-APR-1998
PRIOR APPLICATION NUMBER: PCT/AU98/01023
APPLICATION NUMBER: PCT/AU98/01023
ATTORNEY/AGENT INFORMATION:
NAME: MODITOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/POCKET NUMBER: 32,430
REFERENCE/POCKET NUMBER: 27340-20021.
TELECHOUNE: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650---
TELEFAX: 650---
; INFORMATION FOR SEQ ID NO: 726:
; SEQUENCE CHARACTERISTICS:
. LENGTH: 1974 base pairs
...vpg: nucleic acid
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MOLECULE TYPE: DNA (genomic)
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LOCATION: 1...1974
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
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US-09-252-991A-7065/c
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US-09-221-017B-726
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Sequence 3420, Application US/09489039A

Sequence 3420, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 3420
ILBRICH: 939
                                                                                                  Sequence 19421, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19421
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.3%; Score 17.2; DB 4; Length 534; 86.4%; Pred. No. 75; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.3%; Score 17.2; DB 4; Length 939; Best Local Similarity 73.3%; Pred. No. 87; Matches 22; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09741238
Patent No. 6706867
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOTENZ, Matthias
TITLE OF INVENTION: DNA Array Sequence Selection
Patent No. 6706867
FILE REFERENCE: NIH-05076
CURRENT APPLICATION NUMBER: US/09/741,238
CURRENT PILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-19421
204 GAAGTTCTTGTTAGGAGCGATA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GAGGATCTTGTCAGGAGCGATA 24
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Drosophila melanogaster
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US-09-489-039A-3420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.4%
.---hes 19; Conservative
                                                                       RESULT 22
US-09-270-767-19421
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US-09-489-039A-3420
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVERTION: Reference: 7326-094
CURRENT APPLICANTON NUCLAIC S126-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4139
LENGTH: 534
                                                                                                                                                                                                       APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.

ITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961

FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 25301

LENGTH: 351
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Best Local Similarity 86.4%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.3%; Score 17.2; C
Best Local Similarity 73.3%; Pred. No. 68;
Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3063 GAGGATCCCGTCATGACCGATAACCTG 3037
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CTHER INFORMATION: n means any nucleotide
US-09-270-767-4139
                                                                                                              Sequence 25301, Application US/09513999C; Patent No. 6783961; GRNEAL INFORMATION: APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GAGGATCTTGTCAGGAGCGATA 24
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: 8=g or c
US-09-513-999C-25301
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LOCATION: 345
OTHER INFORMATION: n=a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 148
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                                                                  RESULT 20
US-09-513-999C-25301
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APPLICANT: COLLESI, Chiara
APPLICANT: COLLESI, Chiara
APPLICANT: CASELLI, Chiara
APPLICANT: COMOGLIO, Paolo
TITLE OP INVENTION: RECOMBINANT PROTEINS DERIVED FROM HGF AND MSP
FILE REFERENCE: 0471-0162P
CURRENT APPLICATION NUMBER: US/09/600,991
NUMBER OF SEQ ID NOS: 201-08-20
SOFTWARE: Patentin version 3.1
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APPLICANT: COLLESI, Chiara
APPLICANT: COLLESI, Chiara
APPLICANT: CASELLI, Gianfranco
APPLICANT: CASELLI, Gianfranco
APPLICANT: CASELLI, Gianfranco
APPLICANT: CASELLI, Gianfranco
TITLE OF INVENTION: RECOMBINANT PROTEINS DERIVED FROM HGF AND MSP
FILE REFERENCE: 0471-0162P
CURRENT APPLICATION NUMBER: US/09/600,991
CURRENT APPLICATION NUMBER: US/09/600,991
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                DB 4; Length 1492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.3%; Score 17.2; DB 4; Length 1692; Best Local Similarity 73.3%; Pred. No. 1e+02; Matches 22; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                             8; Indels
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                                                                                                                                                                                                                                                                                                 725 radedercererereadededearaceree 696
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                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                             57.3%; Score 17.2; 73.3%; Pred. No. 97
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Patent No. 6551991
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09600991
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE;
; OTHER INFORMATION: Metron F-1
US-09-600-991-21
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                                                                                                                                                                                   Similarity 73.3
22; Conservative
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APPLICANT: MEDICO, Enzo
                                                                  TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
US-09-600-991-21/c
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                                               1492
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LENGTH: 1692
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LENGTH: 1709
                                                                                                             US-09-741-238-11
                       SEQ ID NO 11
                                                                                                                                                             Query Match
                                                                                                                                                                                        Best Local
Matches 2
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OTHER INFORMATION: This sequence is a variant where two regions OTHER INFORMATION: were found to be deleted when compared to SEQ ID NO:1. PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 2021
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                                                Gaps
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                                                                                                                                                                                                                                                                                                              growth factor and its cDNA and
Score 17.2; DB 4; Length 1709;
Pred. No. 1e+02;
0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.3%; Score 17.2; DB 1; Length 2021; 73.3%; Pred. No. 1e+02; ive 0; Mismatches 8; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                     STATE: Ohio
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    800 Kb
                                                                                                                           705 rccaccacricccccccccaacccccccccc
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                                                                                      1 TCGAGGATCTTGTCAGGAGCGATAGGCTGC 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,925A
FILING DATE: 19920514
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Gregory
REGISTRATION NUMBER: 29,945
REFERENCE/DOCKET NUMBER: CMC 57
TELEPHONE: (513) 241-2324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 45202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.3
                                                                                                                                                                                                                          Sequence 3, Application US/07882925A
Patent No. 5315000
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a
TITLE OF INVENTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: no
    Query Match 57.3%;
Best Local Similarity 73.3%;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (513) 421-7269
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2021 base pairs
TYPB: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 73.3
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: human
DEVELOPMENTAL STAGE:
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: CDNA
CLONE: #19
POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no
ORIGINAL SOURCE:
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APPLICANT: MEDICO, Enzo
APPLICANT: MICHIELI, Paolo
APPLICANT: COLLESI, Chiara
APPLICANT: COLLESI, Chiara
APPLICANT: CONSELLI, Gianfranco
APPLICANT: CONGLIO, Paolo
ITILE OF INVENTION: RECOMBINANT PROTEINS DERIVED FROM HGF AND MSP
ILLE REFERENCE: 0471-0162P
CURRENT APPLICATION NUMBER: 105/09/600,991
CURRENT FILING DATE: 2001-08-20
MUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
IENGTH: 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09601040A
; Sequence 11, Application US/09601040A
; Patent No. 6730657
; GANERAL INFORMATION:
; APPLICANT: MEDICO, Enzo et al.
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
; TITLE OF INVENTION: Recombinant Proteins from HGF and MSP
; CURRENT APPLICATION NUMBER: US/09/601,040A
; CURRENT FILING DATE: 2000-09-08
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-601-040A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.3%; Score 17.2; DB 4; Best Local Similarity 73.3%; Pred. No. 1.1e+02; Matches 22; Conservative 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(2136)
; OTHER INFORMATION:
US-09-600-991-19
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PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 2021
US-08-184-012C-3
                                                                                                                                                                                     RESULT 28
US-08-184-012C-3/C
Sequence 3, Application US/08184012C
Fatent No. 5606029
GENERAL INFORMATION:
TITLE OF INVENTION: Gene for a growth factor and its cDNA and TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
REGIET Wood, Herron & Evans, 2700 Carew Tower
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.3%; Score 17.2; DB 1; Length 2021; Best Local Similarity 73.3%; Pred. No. 1e+02; Matches 22; Conservative 0; Mismatches 8; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 45202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.2
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,012C
FILING DATE: 1/18/94
CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
NAME: Lunn, Gregory
REGISTRATION NUMBER: 29,945
REFERENCE/DOCKET NUMBER: 29,945
REFERENCE/CONTUNICATION INPORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2021 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOUSCULE TYPE: CDNA to mRNA
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CHROMOSOME/SEGMENT: human 3p21/D3F15S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              experimental
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TISSUE TYPE: liver
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ORIGINAL SOURCE:
ORGANISM: human
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LIBRARY: CDNA
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Sequence 4, Application US/07882925A
Patent No. 5315000
GENERAL INFORMATION:
APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a growth factor and its CDNA and
TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSEE: Gregory Lunn STREET: Wood, Herron & Evans, 2700 Carew Tower CITY: Cincinnati Ohio : USA ZIP: 45202 STATE: OF

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Sequence 19, Application US/09600991; Patent No. 6551991; GENERAL INFORMATION:

RESULT 29 US-09-600-991-19/c

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Sequence 2, Application US/0866082B
Patent No. 516770
GENERAL INFORMATION:
APPLICANT: YOSHIKAWA, WATARU
APPLICANT: TAKEHARA, TOYOHIRO
APPLICANT: TAKEHARA, MCHIO
TITLE OF INVENTION: MACROPHAGE STIMULATING PROTEIN VARIANT AND
TITLE OF INVENTION: METHOD FOR PRODUCING THE SAME
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCGAGGATCTTGTCAGGAGCGATAGGCTGC 30
                   CLASSIPICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Gregory
REGISTRATION NUMBER: 29,945
REFERENCE/DOCKET NUMBER: CMC 57
TELECHONNICATION INFORMATION:
TELECHONE: (513) 241-2324
TELEFRAX: (513) 421-7269
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2188 base pairs
LENGTH: 2188 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TYPE: TYPE: GDNA tO MRNA
ANTI-SENSE: nO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             ORGANISH: C57BL/6
BEVELOPMENTAL STAGE:
  FILING DATE: 1/18/94
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
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US-08-666-082B-2/c
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-184-012C-4
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US-08-184-012C-4/c
; Sequence 4, Application US/08184012C
; Patent No. 5606029
; GENERAL INFORMATION:
; APPLICANT: Degen, Sandra J. F.
; TITLE OF INVENTION: protein
; VINBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS: 10
; GREGOTY Lunn
; STREET: Wood, Herron & Evans, 2700 Carew Tower
CITY: Clincinnati
; STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.3%; Score 17.2; DB 1; Length 2188; 73.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: experimental PUBLICATION INFORMATION: RELEVANT RESIDUES IN SEQ ID NO: 4: 1 TO 2188
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.2
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,012C
                       800 Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 rcraggaacrrrrcaggcrggaagggrgc 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: MLS-2
POSITION IN GENOME:
CHROMOSOME/SEGMENT: mouse 9, Hgfl locus
MAP POSITION: Trf-Gnai-2-Hgfl-Cck
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 80(
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.3
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,925A
FILING DATE: 19920514
CLASSIFICATION: 330
ATTORNEY/AGENT INFORMATION:
NAME: LUUN, GPEGOTY
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (513) 241-2324
TELEFRX: (513) 421-7269
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2188 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: mouse
STRAIN: C57BL/6
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: liver
IMMEDIATE SOURCE:
LIBRARY: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA to mRNA
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Best Local Similarity 73.33
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: line:
MOLECULE TYPE: cl
ANTI-SENSE: no
ORIGINAL SOURCE:
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OTHER INFORMATION: Includes five polymorphisms at the nucleotide OTHER INFORMATION: level; one of which results in an amino acid substitution (nuc OTHER INFORMATION: 619). Sequence ID NO:2: contains the identical sequence with OTHER INFORMATION: polymorphic amino acid.

PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2219
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Patent No. 5315000
GENERAL INFORMATION:
APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a growth factor and its cDNA and
TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gregory Lunn
STREET: Wood, Herron & Evans, 2700 Carew Tower
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.3%; Score 17.2; DB 1; Length 2219; Best Local Similarity 73.3%; Pred. No. 1.1e+02; Matches 22; Conservative 0; Mismatches 8; Indels 0
          ORGANISM: human
DEVELOPMENTAL STAGE: fetal
TISSUE TYPE: liver
IMMEDIATE SOURCE:
LIBRARY: cDNA
CLIONE: #33333
POSITION IN GENOME:
CHROMOSOME/SEGMENT: human 3p21/D3F15S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          800 Kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Macintosh COMPUTER: Apple Macintosh COPERATING SYSTEM: Macintosh 6.0.3 SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/07/882,925A FILING DATE: 19920514 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Lunn, Gregory REGISTRATION NUMBER: 29,945 REFERENCE/DOCKET NUMBER: CMC 57 TELECOMMUNICATION INFORMATION: TELEPHONE: (513) 241-2324 TELECOMMUNICATION INFORMATION: TELEPHONE: (513) 421-2324 TELECOMMUNICATION INFORMATION: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: MATTOR ANTHER PARE PARE PARE PAIRS
                                                                                                                                                                                                                                                      experimental
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE:
TISSUE TYPE: liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTI-SENSE:
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APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a growth factor and its cDNA and
TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gregory Lunn
STREET: Wood, Herron & Evans, 2700 Carew Tower
CITY: Cincinnati
STRIE: VISA
STATE: Ohio
COUNTRY: USA
ZIP: 45202
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.3%; Score 17.2; DB 2; Length 2216; Best Local Similarity 73.3%; Pred. No. 1.1e+02; Matches 22; Conservative 0; Mismatches 8; Indels 0
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SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/882,925A
FILING DATE: 19920514

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Gregory

REGISTRATION NUMBER: 29,945

REGISTRATION NUMBER: 29,945

REGISTRATION NUMBER: 29,945

REGISTRATION NUMBER: 29,945

REJECOMMUNICATION INFORMATION:

TELEPHONE: (513) 241-2324

TELEPHONE: (513) 241-7269

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2219 base pairs

TYPE: NUCLEIC ACID

STRANDENESS: single
APPLICATION NUMBER: JP 7-153309
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ROBERT INFORMATION:
REFERENCE/FOCKET NUMBER: 27555
REGISTRATION NUMBER: 27555
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 2216 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6.0.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/07882925A Patent No. 5315000
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: sig peptide LOCATION: 1..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..2133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: 1...2
US-08-666-082B-2
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ORIGINAL SOURCE:
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US-07-882-925A-1/c
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Includes five polymorphisms at the nucleotide level; one of which results in an amino acid substitution (nuc 619). Sequence ID NO:2: contains the identical sequence with
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a growth factor and its CDNA and
TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gregory Lunn
STREET: Wood, Herron & Evans, 2700 Carew Tower
CITY: Cincinnati
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                                                                                                                                                                                                                                                                                                      57.3%; Score 17.2; DB 1; Length 2219; 73.3%; Pred. No. 1.1e+02; ive 0; Mismatches 8; Indels 0.
                                                                                                          Patent No. 5606029
. OTHER INFORMATION: polymorphic amino acid.
. PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCGAGGATCTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 45202
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.2
SOFTWARE: Microsoft Word 5.1
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/184,012C
FILING DATE: 1/18/94
CLASSIFTCATION: 536
ATTONNEY, AGENT INPORMATION:
NAME: Lunn, Gregory
REGISTRATION NUMBER: 29,945
REFRERENS/DOCKT NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human 3p21/D3F15S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08184012C Patent No. 5606029
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                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 73.3
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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          OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 37
US-08-184-012C-2/c
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                                                                                                                                                                                                                                            US-08-184-012C-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY:
                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                     IOD: experimental Includes five polymorphisms at the nucleotide Invelored five polymorphisms at the nucleotide level; one of which results in an amino acid substitution (nu level; one of which contains the identical sequence with 619).
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Sequence 1, Application US/08184012C

Patent No. 5606029

GENERAL INFORMATION:

APPLICANT: Degen, Sandra J. F.

TITLE OF INVENTION: Gene for a growth factor and its cDNA and ITLE OF INVENTION: protein

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Gregory Lunn

STREET Wood, Herron & Evans, 2700 Carew Tower

CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                            57.3%; Score 17.2; DB 1; Length 2219; 73.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 2219
US-07-882-925A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Disakette, 3.50 inch, 800 Kb COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macintosh 7.5.2

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATE: APPLICATION NUMBER: US/08/184,012C

FILING DATE: 1/18/94

CLASSIFICATION: 536

ATTOMNEY/AGENT INFORMATION:
NAME: Lunn, Gregory
REGISTRATION NUMBER: 29,945

REFERENCE/DOCKET NUMBER: CMC 57

TELECOMMUNICATION INFORMATION:
TELERAX: (513) 241-2324

TELERAX: (513) 241-2324

TELERAX: (513) 241-2324

TELERAX: (513) 241-2324

TELERAX: (513) 241-7269

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
TYPE: mucleic acid
STRANDBNESS: single
                                                                                                                                                                                                                                                                                  polymorphic amino acid.
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          CLONE: #33
POSITION IN GENOME:
CHROMOSOME/SEGMENT: human 3p21/D3F15S2
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                                                                                                                                         IDENTIFICATION METHOD: exporther incoration: Includer OTHER INFORMATION: level; OTHER INFORMATION: 619). SOTHER INFORMATION: polymoxi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 73.3 tes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: human
DEVELOPMENTAL STAGE:
TTSSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDN
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 36
US-08-184-012C-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Methods and Kits Using Macrophage Stimulating
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APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a growth factor and its cDNA and
TITLE OF INVENTION: protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCES: ADDRESSE:
ADDRESSEE: Gregory Lunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
57.3%; Score 17.2; DB 5;
Best Local Similarity 73.3%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                800 Kb
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ZIP: 45202
ZIP: 45202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 86
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.3
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
RPLING DATE: 19220514
CLASSIFICATION: 530
TITLE OF INVENTION: Methods and Kits TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-882-925A-7/c
; Sequence 7, Application US/07882925A
; Patent No. 5315000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P09:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
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NAME: Lunn, Gregory
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                 USA
                                                                                                                                                                                                                        94080
                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-13830-1
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08334177
Sequence 1, Application US/08334177
Sequence 1, Application US/08334177
Patent No. 5696086
GENERAL INFORMATION:
APPLICANT: Avraham, Hava Karsenty
APPLICANT: Godowski, Paul J.
TITLE OF INVENTION: Methods and Kits Using Macrophage Stimulating Protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.3%; Score 17.2; DB 1; Length 2232; Best Local Similarity 73.3%; Pred. No. 1.1e+02; Matches 22; Conservative 0; Mismatches 8; Indels 0
                                                                                                                         57.3%; Score 17.2; DB 1; Length 2219; 73.3%; Pred. No. 1.1e+02; tive 0; Mismatches 8; Indels 0
                                                         2: FROM 1 TO 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genentech, Inc.
New England Deaconess Hospital Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,177
         polymorphic amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705 rccaccacricccccccccaaccricc 676
                                                                                                                                                                                                                                                                  679 rcgaggaacrigcccggcrcgaagggagc 650
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                                                                                                                                                                                                                        1 TCGAGGATCTTGTCAGGAGCGATAGGCTGC 30
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: New England Deaconess F
                        PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-184-012C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 912
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-5416
TELEPHONE: 415/952-9881
                                                                                                     Query Match
Best Local Similarity 73.3%
Local Similarity
Local 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-334-177-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 39
PCT-US95-13830-1/c
                                                                                                                                                                                                                                                                                                                                             RESULT 38
US-08-334-177-1/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 241-2324
TELEPHONE: (513) 421-2324
TELEPHONE: (513) 421-2324
TELEPHONE: (513) 421-2324

INFORMATION FOR SED ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2262 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: Intear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Identical to sequence ID NO: 1: with 5' and 3'
DESCRIPTION: adaptors added to make a full-length CDNA
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
DEVELOPMENTAL STACE: fetal
TISSUE TYPE: liver
INMEDIATE SOURCE:
INMEDIATE SOURCE:
ILIBRARY: CDNA
CLONE: #33 including 5' and 3' adaptors
ILIBRARY: CDNA
TELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 2262
US-07-882-925A-7

QUETY MATCH
STANDEDNESS: NO: 1.10+02;
MATCHES 22; CONSERVATIVE 0; Mismatches 8; Indels 0; Gaps 0;
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1 TCGAGGATCTTGTCAGGAGCGATAGGCTGC 30

8 8

Search completed: January 7, 2005, 11:00:37 Job time : 56.2105 secs

Sequence 128, App Sequence 128, App Sequence 134, App Sequence 139, App Sequence 6890, Ap Sequence 90830, Ap Sequence 38152, A Sequence 38152, A Sequence 38179, A Sequence 18174, A Sequence 17, Appli Sequence 7, Appli Sequence 17, Appli Sequence 212, App Sequence 212, App Sequence 212, App Sequence 2214, A Sequence 2381, A Sequence 253, App Sequence 1073, A Sequence 10734, A Sequence 10734, A Sequence 10734, A Sequence 2791, A Sequence 27997, A Sequence 27997, A

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

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Sequence 2, Application US/08940544B

Sequence 2, Application US/08940544B

Publication No. US20020018783A1

GENERAL INFORMATION:
APPLICANT: SADELAIN, MICHEL
APPLICANT: CHEUNG, NAI-KONG V.
APPLICANT: CHEUNG, NAI-KONG V.
TITLE OF INVENTION: FUSION PROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE APPLICATION NUMBER: US/08/940,544B
CURRENT FILING DATE: 1997-09-30
EARLIER FILING DATE: 1997-09-30
SEALIER FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Downstream primer for PCR amplification.
US-08-940-544-2
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17 US-10-437-963-23123
17 US-10-437-963-23123
17 US-10-437-963-23127
17 US-10-437-963-23127
18 US-10-417-375-128
16 US-10-632-983-46
15 US-10-632-983-46
16 US-10-632-983-46
16 US-10-260-238-44
17 US-10-260-238-44
15 US-10-369-493-38650
15 US-10-369-493-38650
15 US-10-369-493-38650
17 US-10-369-493-38079
15 US-10-369-493-38079
17 US-10-369-493-38079
18 US-10-369-493-38079
19 US-10-437-963-67598
10 US-10-437-963-67598
11 US-10-425-115-34877
18 US-10-425-115-34877
19 US-10-425-115-34877
19 US-10-425-115-34877
11 US-09-960-552-10773
12 US-10-625-115-34877
13 US-10-027-632-27997
13 US-10-027-632-27997
13 US-10-027-632-27997
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100.0%; Score 30; DB 8; L
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 30; Conservative 0; Mismatches 0;
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    667
1523
1604
52679
    TYPE: DNA
ORGANISM: HUMAN
    19.4
19.4
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Sequence 1, Appli
Sequence 256, App
Sequence 8, Appli
Sequence 8, Appli
Sequence 2, Appli
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Sequence 98, Appl
Sequence 1316, Ap
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Appli
Sequence 1, Appli
                                                                                                                                          January 7, 2005, 11:00:44; Search time 1275.26 Seconds (without alignments) 134.979 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(gn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US06_PUBGOMB.seq:*
(cgn2_6/ptodata/2/pubpna/US06_PUBGOMB.seq:*
(cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/DS08_NEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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(cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-207-655-98
US-10-641-643-1316
US-10-076-934-1
US-09-997-722-257
US-10-143-238-1
US-09-937-722-256
US-09-997-722-256
US-10-448-256-8
US-10-273-762-2
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                                                                                                                                                                                                                                                                                                                                                                  4293498 seqs, 2868903791 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-940-544-2
US-09-738-546-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Gaps

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                                                                     GENERAL INFORMATION:
APPLICANT: YU, XUB-ZHONG
APPLICANT: YU, XUB-ZHONG
APPLICANT: YU, XUB-ZHONG
APPLICANT: ANASETIT. CLAUDIO
TITLE OF INVENTION: CD28-SPECIFIC ANTIBODY COMPOSITIONS FOR USE IN METHODS
TITLE OF INVENTION: OF IMMUNOSUPPRESSION
FILE REPRESENCE: FHCC:007US
CURRENT APPLICATION NUMBER: 40/9/138,546
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 60/170,857.
PRIOR PILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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68.0%; Score 20.4; DB 11; Length 1514;
Best Local Similarity 95.5%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 1514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOS-09-185-594-7/
US Sequence 7, Application US/09836544

Publication No. US2004007228341

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Rapid Immunoselection Cloning Method

FILE REFERENCE: 11-88L

CURRENT APPLICATION NUMBER: US/09/836,544

CURRENT PILING DATE: 2001-04-17

PRIOR PILING DATE: 1992-12-01

PRIOR PILING DATE: 1990-07-13

PRIOR PILING DATE: 1998-00-13

PRIOR PILING DATE: 1998-00-13

PRIOR PILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 7

LENGTH: 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.5%; Pred. No. 23
Matches 21; Conservative 0; Mismatche
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US-09-738-546-1/c
; Sequence 1, Application US/09738546
; Patent No. US20020006403A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-738-546-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (100)..(759)
US-09-836-544-7
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US-J0-207-655-98/C
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US-09-836-544-7/c
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LENGTH: 1514
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Sequence 1316, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Sellhamer
TITLE OF INVENTION:
GENE EXPRESSION
; Sequence 98, Application US/10207655
; Publication No US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.;
; TITLE OF INVENTION: BINDING DOWAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT PILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 98
LENGTH: 1514
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MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: TEM PC COMPACIDE
COMPUTER: TEM PC COMPACIDE
COMPUTER: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRITY APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION AURKNOWN>
FILING DATE: CURKNOWN>
FILING DATE: CURKNOWN>
APPLICATION NUMBER: CURKNOWN>
APPLICATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.0%; Score 20.4; DB 15; Best Local Similarity 95.5%; Pred. No. 23; Matches 21; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: 9338444
SEQUENCE DESCRIPTION: SEQ ID NO: 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1316:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-10-207-655-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-10-641-643-1316/c
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ch 68.0%; Score 20.4; DB 10;
11 Similarity 95.5%; Pred. No. 23;
21; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           889 CGTGTCAGGAGCGATAGGCTGC 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              889 cerercacaaccaracecrec 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9. CTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 CTTGTCAGGAGCGATAGGCTGC 30
                                        US-10-143-238-1/c
; Sequence 1, Application US/10143238
; Publication No. US20030166502A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-835-297-3/c
; Sequence 3, Application US/09835297
; Publication No. US20030086932A1
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (223)...(885)
US-10-143-238-1
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
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Best Local Similarity
Matches 21; Conserva
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US-09-997-722-256/c
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Sequence 257, Application US/0997722

Publication No. US20040072154A1

Publication No. US20040072154A1

GENERAL INFORMATION:

APPLICANT: Morris, David

APPLICANT: Engelhard, Eric

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REFERENCE: A-71171/RMS/DCF

CURRENT APPLICATION NUMBER: US/09/997,722

CURRENT FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2000-103-02

NUMBER OF SEQ ID NOS: 301

SOFTWARE: PatentIn version 3.1

SEQ ID NO 257

LENGTH: 3804
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                                          DB 16; Length 1514;
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: O'HARA Jr., Richard
APPLICANT: O'HARA Jr., Richard
APPLICANT: Nagelin, Ann Marie
TITLE OF INVENTION: CD28-MEDIATED SIGNALING AND USES THEREFOR
TITLE OF INVENTION: CD28-MEDIATED SIGNALING AND USES THEREFOR
FILE REFERENCE: GNN-0.28
CURRENT APPLICATION NUMBER: US/10/076,934
PRIOR APPLICATION NUMBER: 60/269,756
PRIOR APPLICATION NUMBER: 60/269,756
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRAEKSEQ for Windows Version 4.0
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                                        68.0%; Score 20.4; D
95.5%; Pred. No. 23;
cive 0; Mismatches
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0; Mismatches
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Pred. No. 23
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                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/10076934; Publication No. US20030170232A1; GENERAL INFORMATION:
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Best Local Similarity 95.5%;
Matches 21; Conservative (
                                        Query Match 68.0
Best Local Similarity 95.5
Matches 21; Conservative
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US-10-641-643-1316
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US-10-076-934-1/c
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LENGTH: 3803
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APPLICANT: Griffin, Mathew
APPLICANT: Griffin, Mathew
APPLICANT: Kranz, David
TITLE OF INVENTION: GREACE-BOUND ANTIGEN BINDING PORTIONS OF ANTIBODIES
TITLE OF INVENTION: THAT BIND TO CTLA4 AND USES THEREFOR
FILE REFERENCE: GNN-0140P
CURRENT APPLICATION NUMBER: US/09/835,297
PRIOR PILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTING DATE: 200-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shaw, Andrey S.
TITLE OF INVENITON: DIFFERENTIAL REGULATION OF T CELL SURVIVAL AND TITLE OF INVENITON: PROLIFERATION
FILE REFERENCE: GNN-030
CURRENT APPLICATION NUMBER: US/10/143,238
CURRENT APPLICATION NUMBER: US/202-05-10
PRIOR FILING DATE: 2002-05-10
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
ILENGTH: 3804
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LENGTH: 1329
                                                                                                                                  TYPE: DNA
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APPLICANT: CHEUNG, Nai-Kong V
TITLE OF INVENTION METHOD FOR PREPARATION OF SINGLE CHAIN ANTIBODIES
FILE REFERENCE: 676-A-PCT
CURRENT APPLICATION NUMBER: US/10/273,762
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/330,396
PRIOR FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 10/97,558
PRIOR FILING DATE: 2002-03-08
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APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-103-02
NUMBER OF SEQ ID NOS: 301
SEQ ID NO 256
LENGTH: 51365
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Publication No. US20040043401A1

GENERAL INFORMATION:
APPLICANT: Sadelain, Michel
APPLICANT: Brentjens, Renier
APPLICANT: Maher, John
TITLE OF INVENTION: Chimeric T Cell Receptors
FILE REFERENCE: MSK.P-058
CURRENT FILING DATE: 2003-05-28
CURRENT FILING DATE: 2003-05-28
FRIOR FILING DATE: 2002-05-28
NUWBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 36
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Pred. No. 26;
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88.0%; Pred. No. 24;
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1 Similarity 95.5%;
21; Conservative (
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                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-09-997-722-256
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Best Local Similarity
Matches 21, Conserva
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Best Local Similarity
Matches 22; Conserv
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US-10-448-256-8
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US-10-273-762-2
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Pind
APPLICANT: Li, Pind
APPLICANT: Li, Pind
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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Pred. No. 64;
0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_28233C.1
US-10-437-963-23123
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PRIOR APPLICATION NUMBER: PCT/US01/32565
PRIOR FILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 2
LENGTH: 32
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 79.3%;
Matches 23; Conservative
                                                                                                                                    , ORGANISM: Homo Sapiens
US-10-273-762-2
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    Length 430442;
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                                            Indels
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Sequence 46, Application US/10632983

Publication No. US20040067518A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 36 Human Secreted Proteins

FILE REFERENCE: PZO2591C1D1

CURRENT PELICATION NUMBER: US/10/632,983

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: OS/716,129

PRIOR APPLICATION NUMBER: PCT/US99/03939

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1998-02-26

PRIOR FILING DATE: 1998-02-26

PRIOR PLING DATE: 1998-02-26
Query Match, 64.7%; Score 19.4; DB 18;
Best Local Similarity 79.3%; Pred. No. 82;
Matches 23; Conservative 0; Mismatches 6;
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (20)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
LOCATION: (375)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
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PRIOR APPLICATION NUMBER: 60/076,054
PRIOR FILING DATE: 1998-02-26
PRIOR APPLICATION:
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                                            Matches
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 28652
LENGTH: 4509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.7%; Score 19.4; DB 17; Length 4509; 79.3%; Pred. No. 68; tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                            Length 4467;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION NOVel Therapeutic Targets in Cancer
FILE REPRENCE: 520452001600
CURRENT APPLICATION NUMBER: US/10/417,375
CURRENT PILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                            Query Match 64.7%; Score 19.4; DB 17;
Best Local Similarity 79.3%; Pred. No. 68;
Matches 23; Conservative 0; Mismatches 6;
                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT4530_28237C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT4530_3322C.1
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                                                                                                                                                                                                                                                                                  2 CGAGGATCTTGTCAGGAGCGATAGGCTGC 30
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La ROBa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 23127
LENGTH: 4467
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Matches 23; Conservative
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CRGANISM: Homo sapiens
US-10-417-375-128
                                                                TYPE: DNA
ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-437-963-28652/c
                                                                                                                                                      US-10-437-963-23127
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LENGTH: 430442
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US-10-417-375-128
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                                                                                                            FEATURE:
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us-09-786-502a-8.rnpb

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Kreps, Joel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 21
US-10-424-599-90830
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APPLICANT:
APPLICANT:
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US-10-19-991-6890/c
Sequence 6890, Application US/10719993
Sequence 6890, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE PRILES PRESENCE
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; Publication No. US20030219745A1
; GENERAL INFORNATION:
    APPLICANT: Tang, Y. Tom
    APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802CON
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/774,528
FRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: PL_Genes Version 2.0
; SEQ ID NO 129
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.3%; Score 19; DB 16; Length 1189; Best Local Similarity 81.5%; Pred. No. 97; Matches 22; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 GAGGATTTTGCCAGGTGGGATGGGCTG 335
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PRIOR FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn version 2
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; LOCATION: (167)..(4381)
US-10-120-988-129
                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo.sapiens
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-120-988-129/c
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                                                                                                                            SEQ ID NO 46
LENGTH: 1189
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(303172)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-719-993-6890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 90830, Application US/10424599

Publication No. US20040031072A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 39-21 (53233) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 90830
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APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ann, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 6011.NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,77
PRIOR FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
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                                                                                                                                                                          Query Match 63.3%; Score 19; DB 18; Length 303172; Best Local Similarity 81.5%; Pred. No. 1.2e+02; Matches 22; Conservative 0; Mismatches 5; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53030C.1
US-10-424-599-90830
                                                                                                                                                                                                                                                                                                                                                           299749 regagearcricicadaacreaaacac 299723
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Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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Goff, Stephen A.
Katagiri, Fumiyak
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Sequence 38204, Application US/10369493
; Sequence 38204, Application US/10369493
; Publication No. US203033675A1
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
    APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38204
                                                                                                                                                                                                                                                        ## Sequence 38079, Application US/10369493
### Septicant: Cao, Yongwei
### APPLICANT: Slater, Steven C.
### APPLICANT: Slater, Steven C.
### APPLICANT: Chen, Xianfeng
### TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
### TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
### TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
### CURRENT APPLICATION NUMBER: US/10/369,493
### CURRENT PILING DATE: 2003-02-28
### PRIOR PILING DATE: 2003-02-21
### PRIOR PILING DATE: 2003-02-21
### NUMBER OF SEQ ID NOS: 47374
### SEQ ID NO 38079
### LENGTH: 630
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          Length 630;
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                                                        Indels
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     Score 18.8; DB 15;
Pred. No. 1.2e+02;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.7%; Score 18.8; DB 15; Best Local Similarity 76.7%; Pred. No. 1.2e+02; Matches 23; Conservative 0; Mismatches 7;
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Best Local Similarity 76.7%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38079
     Query Match
Best Local Similarity 76.7%;
Matches 23; Conservative (
                                                                                                                                                                                                                                                     US-10-369-493-38079
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Sequence 35152, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Galdman, Barry
APPLICANT: Goldman, Barry
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
FRIOR PRILING DATE: 2002-02-21

WUMBER OF SEQ ID NOS: 47374

SEQ ID NO 35152

LENGTH: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 38650
LENGTH: 609
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                                                                                                                                                                              Length 542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 62.7%; Score 18.8; DB 15; Best Local Similarity 76.7%; Pred. No. 1.2e+02; Matches 23; Conservative 0; Mismatches 7;
                                                                                                                                                                              Score 18.8; DB 16;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 rcgrcgarcrrgrcageccggararrcrgc 232
                                                                                                                                                                         Query Match 62.7%; Score 18.8; D
Best Local Similarity 90.9%; Pred. No. 1.2e
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TCGAGGATCTTGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 23
US-10-369-493-38650
Sequence 38650, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           519 CGACGATCTTGGCAGGAGCGAT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Agrobacterium tumefaciens US-10-369-493-38650
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                                                                                                                                                                                                                                                                          2 CGAGGATCTTGTCAGGAGCGAT 23
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 441
LENGTH: 542
                                                                            ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-441
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US-10-369-493-35152
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; Sequence 67598, Application US/10437963
; Publication No. US20040123343A1
GENERAL INPORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Broad With Street Boukharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67598
LENGTH 2115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 7, Application US/10273762 |
| Sequence 7, Application US/10273762 |
| Publication No. US20030147881A1 |
| GENERAL INFORMATION: |
| APPLICANT: CHEUGA Nai-Kong V |
| APPLICANT: GUO, Hong-fen |
| TITLE OF INVENTION: METHOD FOR PREPARATION OF SINGLE CHAIN ANTIBODIES |
| TITLE OF INVENTION: METHOD FOR PREPARATION OF SINGLE CHAIN ANTIBODIES |
| TITLE OF INVENTION: WETHOR FOR TOWN OF SINGLE CHAIN ANTIBODIES |
| TITLE OF INVENTION NUMBER: US/10/273,762 |
| PRIOR FILING DATE: 2002-10-17 |
| PRIOR FILING DATE: 2002-03-08 |
| PRIOR FILING DATE: 2002-03-08 |
| PRIOR FILING DATE: 2002-03-08 |
| PRIOR PRILING DATE: 2001-10-18 |
| NUMBER OF SEQ ID NOS: 17 |
| SEQITWARE: Patentin version 3:1 |
| SEQITUARE: Patentin version 3:1 |
| TRNCTH: AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.7%; Score 18.8; DB 17;
Best Local Similarity 76.7%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: PAT_MRT4530_6843C.1
US-10-437-963-67598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1517 TCGAGGATCTTATCAAGACAAATATGGTGC 1546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 TGTCAGGAGCGATAGGCTGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapiens
US-10-273-762-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Oryza Bativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
US-10-172-118-212/c
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                                                                                          Sequence 48174, Application US/10437963
; Sequence 48174, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION VUMBER: US/10/437,963
; CURRENT APPLICANION VUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-65-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 48174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.7%; Score 18.8; DB 17; Length 815; Best Local Similarity 90.9%; Pred. No. 1.2e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_50875C.1
US-10-437-963-48174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638 TCGAGGATCTTGTCGGGATCGA 617
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US-10-437-963-67598
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FEATURE:
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Sequence 212, Application US/10342887

Publication No. US20040058340A1

GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Linsley, Peter S.
APPLICANT: Roberts, Christopher J.
APPLICANT: Roberts, Christopher J.
APPLICANT: Nao, Mao
APPLICANT: Nao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Nao 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Daisnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887

CURRENT FILING DATE: 2001-06-18

PRIOR PILING DATE: 2001-06-18

PRIOR PILING DATE: 2002-05-14

PRIOR PILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

SEQ ID NO 212

LENGTH: 2609
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                                                                                                          APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernarda, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
PRIOR APPLICATION NUMBER: 06/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 61.3%; Score 18.4; DB 15; Length 2609; Best Local Similarity 78.6%; Pred. No. 1.9e+02; Matches 22; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1670 GAGCATCTTTTCAGGATGGATGGACTGC 1643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK000345
DATABASE ENTRY DATE: 2001-06-18
                                                                                                        Dai, Hongyue
He, Yudong
Linsley, Peter
                                                                     Mao, Mao
Roberts, Chris
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 32
US-10-342-887-212/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-342-887-212
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                                               APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 34870, Application US/10425115
; Sequence 34870, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: NUMBER: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 34870
; LENGTH: 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.3%; Score 18.4; DB 15; Best Local Similarity 78.6%; Pred. No. 2.2e+02; Matches 22; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

: LOCATION: (4187715)

: OTHER INFORMATION: a, t, c, g, other or unknown

US-10-156-761-1
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GENERAL INCORMATION:
CENERAL INFORMATION:
CURRENT HARTORY
CURRENT APPLICANT:
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
CHORN REPUBLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-06-30
CHORN RELING DA
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ORGANISM: Streptomyces avermitilis
FRATURE:
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ORGANISM: Zea mays
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RESULT 35 US-10-425-114-22914

RESULT 33

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Sequence 10773, Application US/09960352

Patent No. US20020137139A1

GENERAL INCOMMATION:
APPLICANT: Waster, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Wagappan
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.7%; Score 18.2; DB 13; Length 52679; Best Local Similarity 87.0%; Pred. No. 2.7e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 328;
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Pred. No. 2.6e+02;
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US-10-448-256-6/C

Sequence 6, Application US/10448256

Publication No. US20040043401A1

GENERAL INFORMATION:
APPLICANT: Sadelain, Michel
APPLICANT: Brentjens, Renier
APPLICANT: Maher, John
TITLE OF INVENTION: Chimeric T Cell Receptors
FILE REPRENCE: MSK. P-058

CURRENT PILING DATE: 2003-05-28

CURRENT FILING DATE: 2002-05-28

PRIOR FILING DATE: 2002-05-28

PRIOR FILING DATE: 2002-05-28

SOFTWARE: Patentin version 3.2

SEQ ID NO 6

LENGTH: 328

TYDE: NAT
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100.0%; Pred. No. 2...
... 0; Mismatches
                    CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SEQ ID NO 553
LENGTH: 52679
TYPE: DNA
ORGANISM: MUS musculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1240 AGGATTTTGGCAGGAGCAATAGG 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AGGATCTTGTCAGGAGCGATAGG 26
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, OTHER INFORMATION: n = A,T,C or G
US-10-087-192-553
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      FILE REFERENCE: 529452000122
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Best Local Similarity 100.º
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: human
US-10-448-256-6
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                                                            Sequence 13.957, Application US/10425115
Sequence 13.867, Application US/10425115
Publication No. US20040214272A1
Septembran INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cav, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 [5322] B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 34867
LENGTH: 1604
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US-10-087-192-553
US-10-087-192-553
; Sequence 553, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ; TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Clone ID: LIB3592-068-C8_FLI
US-10-425-114-22914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_131801C.1 US-10-425-115-34867
Sequence 22914, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
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Matches 20; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
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US-10-027-632-107348

i Sequence 107348 Application US/10027632

j Bublication No. US20020198371A1

GENERAL INFORMATION:

I TILE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: 108027.129

CURRENT FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-24

PRIOR PRIUM APPLICATION NUMBER: US 60/193,483

PRIOR PRIUM DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-18

PRIOR PRIUM DATE: 1999-09-18

PRIOR PRIOR DATE: 1999-09-18

PRIOR PRIOR DATE: 1999-09-18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0%; Score 18; DB 9; Length 388; Best Local Similarity 80.8%; Pred. No. 2.7e+02; Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                      TYPE: DNA | TYPE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCGAGGATCTTGTCAGGAGCGATAGG 26
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NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10773
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.0
Best Local Similarity 80.8
Matches 21; Conservative
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US-10-027-632-107348
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25 19.4 64.7 466 9 CL702561 CL702561 SPEARED DAGES2667 AQ652667 Sheared DAGES2667 Sheared DAGES267 Sheared DAGES27 Sheared DAGES27 </th <th>ALIGNMENTS RESULT 1 ROB1334</th> <th>BOBB1384 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS DEFINITION 1030036A05.yl C. reinhardtii CC-1690, Deflagellation (normalized), Locus Locus ACCESSION BOB13384. GI:22059341 KEYWORDS EXT. Chlamydomonas reinhardtii ORGANISM Chlamydomonas reinhardtii AUTHORS Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unscular Plants. Project: 1030 JOURNAL Unpublished (2002)</th> <th>Contac DCMB F DUME U Durhan Tel: S Fax: S Email:</th> <th>/BITAINTE—"CV-1690 WING Cype mc+ 11gr // BITAINTE—"CV-1690 WING Cype mc+ 11gr // Clone lib="C. reinhardtii CC-1690, Deflagellation // Clone lib="C. reinhardtii CC-1690, Deflagellation // Clone lib="C. reinhardtii CC-1690, Deflagellation // Note liberallation library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells which had been re-synthesizing flagella for 15, 30 and 60 min after being deflagellated by pH shock. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II // Stratagene) in the ECORI (9) and XhoRI (3) sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."</th>	ALIGNMENTS RESULT 1 ROB1334	BOBB1384 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS DEFINITION 1030036A05.yl C. reinhardtii CC-1690, Deflagellation (normalized), Locus Locus ACCESSION BOB13384. GI:22059341 KEYWORDS EXT. Chlamydomonas reinhardtii ORGANISM Chlamydomonas reinhardtii AUTHORS Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unscular Plants. Project: 1030 JOURNAL Unpublished (2002)	Contac DCMB F DUME U Durhan Tel: S Fax: S Email:	/BITAINTE—"CV-1690 WING Cype mc+ 11gr // BITAINTE—"CV-1690 WING Cype mc+ 11gr // Clone lib="C. reinhardtii CC-1690, Deflagellation // Clone lib="C. reinhardtii CC-1690, Deflagellation // Clone lib="C. reinhardtii CC-1690, Deflagellation // Note liberallation library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells which had been re-synthesizing flagella for 15, 30 and 60 min after being deflagellated by pH shock. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II // Stratagene) in the ECORI (9) and XhoRI (3) sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
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n 5.1.6 Compugen Ltd. Compugen Ltd. ; Search time 1791.05 Seconds (without alignments) 610.363 Million cell updates/sec gctgc 30 residues meters: 65645750		ed by chance to have a f the result being printed, ore distribution.	Description B0813384 1030036A0 B0813384 1030036A0 CD488918 T16 B08 T B0715651 AGENCOURT CE517324 tigr-gss- CA655944 wlmo.pk00 CL155659 104 342 1 BP7000570 BP700670	CA17252 CSGSEALUO BH051040 RPCI -24-3 CA610501 wrl.pk011 BZ47621 BONDV41TF BF046684 BP250020A CF82870 tric087xj AZ216274 Sheared D CB909216 tric087xj CF87769 tric087xj CF87769 tric034xf BH504182 BOGQW35TF BH650178 BOGQW35TF CL701378 SP CA771378 CCF87750 tric034xf CL701378 CCF877920 tric034xf CL701378 CCF877920 tric034xf CA7713582 AMGNNUC:N AJ706082 AJ706082
GenCore version 5.1 Copyright (c) 1993 - 2005 Compount of the compount of the compount of the content of the	000000000 Match 0% Match 100% first 45 summarie	Database: EST:* 1: 9D est1:* 2: 9D est2:* 3: 9D htc:* 4: 9D est3:* 5: 9D est5:* 6: 9D est5:* 7: 9D est6:* 8: 9D 9881:* 9: 9D 9881:* 9: 9D 9881:* 9: 9D 9881:* and is derived by analysis of the total score and is derived by analysis of the total score	Score Match Length DB ID 21 70.0 608 5 BQ8 21 70.0 1178 5 BQ7 20.8 69.3 310 9 CES 20.4 68.0 777 5 BP7	C 9 20 66.7 473 BH051040 10 19.6 65.3 505 6 CA610501 2 11 19.6 65.3 505 6 CA610501 2 12 19.6 65.3 636 2 CA610501 2 13 19.6 65.3 636 7 CF882870 2 14 19.6 65.3 771 8 AZ216274 2 15 19.6 65.3 749 6 CB909216 2 16 19.6 65.3 753 7 CF882870 2 19.6 65.3 753 7 CF882870 2 19.6 65.3 753 7 CF882870 2 19.6 65.3 752 8 BH504182 2 19.4 64.7 328 1 AA486214 2 2 19.4 64.7 395 6 CB73582 2 19.4 64.7 395 6 CB73582 2 19.4 64.7 395 6 CB73582

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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; I (bases 1 to 1178)

SS NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapba-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rlad quality sequence stop: 263.
High quality sequence stop: 263.
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The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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( Dases 1 to 310)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 5; Length 1178;
Pred. No. 1.7e+02;
0; Mismatches 5; Indels
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.0%; Score 21; DB Best Local Similarity 82.8%; Pred. No. 1.7e Matches 24; Conservative 0; Mismatches
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Canis familiaris
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BQ715651.
BQ715651.1 GI:21854550
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="caxon:5270"
/cell type="Tellospore"
/dev Eages="Germinating tellospore"
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/lab_host="E. coli"
/clone lib="Tellospore"
/note="Vector: pDNR-LIB; Site_1: SfiltA; Site_2: SfiltB;
/note="Vector: pDNR-LIB; Site_1: SfiltA; Site_2: SfiltB;
/note="Vector: pDNR-LIB; site_indicting tellospores. cDNA was amplified by PCR and unidirectionally cloned into pDNR-LIB
plasmid, with the use of Clontech's Creator SMART cDNA
Library Construction Kit."
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sacadura, N.T. and Saville, B.J. Gene expression and EST analyses of Ustilago maydis germinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Barry J. Saville
Saville Lab
University of Toronto
3159 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
                                                                              Gaps
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Ustilaginomycetidae, Ustilaginales, Ustilaginaceae, Ustilago.
1 (bases 1 to 650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bsaville@utm.utoronto.ca
Seg primer: M13 reverse primer (5' AAACAGCTATGACCATGTTCA 3').
Location/Qualifiers
                                                                                                                                                                                                                                                                  CD488918 ·
T16 B08 Teliospore Ustilago maydis CDNA 5', mRNA sequence.
CD488918
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                                       Length 608;
                                Query Match 70.0%; Score 21; DB 5; Length 608
Best Local Similarity 82.8%; Pred. No. 1.6e+02;
Matches 24; Conservative 0; Mismatches 5; Indels
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                                                                                                                                              2 CGAGGATCTTGTCAGGAGCGATAGGCTGC 30
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/strain="FB1/FB2"
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Ustilago maydis
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BQ715651/c
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Gaps

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finite="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
Sorghum bicolor (sorghum)
Sorghum bicolor
Surghum bicolor
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 777)

Osada,S., Kitayama,A., Ueno,N. and Taira,M.

Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos

Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Sorghum methylation-filtered library (LibID:
                                                                                                                          1 (bases 1 to 736)
Budiman, M.A., Flick, B., Jones, J., Nunberg, A., Citek, R.W.,
Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,
Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.
GeneThresher methylation filtered genomic sequences from Sorghum
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BP700670 Osada Taira anterior neuroectoderm (ANE) pCS105 CDNA
library Xenopus laevis CDNA clone XL490h05ex 5', mRNA sequence.
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Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%; Score 20.4; DB 9; Length 736; 80.0%; Pred. No. 3e+02; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                       bicolor
Unpublished (2004)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
plate: 342 row: a column: 17
Seq primer: M13/pUC Forward
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7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
843: 81-03-5841-4434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .736
/organism="Sorghum bicolor"
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/cultivar="ATx623"
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Location/Qualifiers
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BP700670.1 GI:46049030
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Best Local Similarity 80,00
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                                                                                                                                                                                                                                                                                                                                                                                                                    664 bp mRNA linear EST 24-NOV-2002 wlm0.pk0021.c4 wlm0 Triticum aestivum cDNA clone wlm0.pk0021.c4 5' end, mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Sopramatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 664)

Tingey, S. V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.

Miao, G., Caraher, N. and Hanafey, M.K.

Unpublished (2002)

Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:4565"
/clone="wlm0.pk0021.c4"
/tissue type="leaf"
/clone lib="wlm0"
/note="vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) seedlings 0 hr after
inoculation with Erysiphe graminis f. sp tritici"
                                                                                                                                                                                                          Gaps
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  /db_xref="taxon:9615"
/clone_lib="Dog_Library"
/note="Site_l: BatXI; Libraries were prepared from
peripheral blood"
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E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
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                                                                                                                                                     Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.7%; Score 20.6; DB 6; Length 664;
85.2%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                          Indels
                                                                                                                                                     Query Match 69.3%; Score 20.8; DB 9; Best Local Similarity 91.7%; Pred. No. 1.8e+02; Matches 22; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seg primer: M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               friticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Stephens"
                                                                                                                                                                                                                                                            6 GATCTTGTCAGGAGCGATAGGCTG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .664
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CL155659
CL155659.1 (
GSS.
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FEATURES

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

LOCUS DEFINITION

ACCESSION

CA655944/c

RESULT 5

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RESULT 6 CL155659/c LOCUS DEFINITION

Matches

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ORIGIN

ACCESSION VERSION KEYWORDS

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Gaps ö

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Length 320;
Query Match 66.7%; Score 20; DB 6; Le:
Best Local Similarity 82.1%; Pred. No. 4.1e+02;
Matches 23; Conservative 0; Mismatches 5;
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                                                                                                                                                                                                        225 gagcarctrercaagagcaaaacgcrec 252
                                                                                                                                       3 GAGGATCTTGTCAGGAGCGATAGGCTGC 30
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="RPCI-24-397C22"
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82.18;
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Best Local Similarity 82.1
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharum officinarum
Saccharum officinarum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 bp mRNA linear EST 24-SEP-2003
SB1 Saccharum officinarum cDNA clone SCSGSB1008H04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 008 row: H column: 04
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                          /tissue_type="anterior neuroectoderm" | dev stage="late gastrula (stage 12.5)" | /clone_llate gastrula (stage 12.5)" | /clone_lla="loada Taira anterior neuroectoderm (ANE) | pCS105 cDNA library"
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Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.0%; Score 20.4; DB 5; Length 777; 80.0%; Pred. No. 3.1e+02; ive 0; Mismatches 6; Indels (
Bmail: m_taira@biol.s.u-tokyo.ac.jp,
URL:http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.
Location/Qualifiers
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                                                                                                                                          /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL490h05ex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCGAGGATCTTGTCAGGAGCGATAGGCTGC 30
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/db_xref="taxon:4547"
/clone="SCSGSB1008H04"
/lab_host="DH10B"
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SCSGSB1008H04.g SB1
5', mRNA sequence.
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CA172592
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SOURCE

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ORIGIN

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Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSS: RPCI-24-397C22.TJ
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bacpac/orderingframe.htm). BAC end
Plate: 397 row: C column: 22
Seq primer: T7
Class: BAC ends.
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/cell type="Spleen/Brain"
/coll type="Spleen/Brain"
/clone_lib="RPCI-24"
/clone_lib="RPCI-24"
/note="Vector: PTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: PTARBAC1; Site_1: BamH1; SPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the PTARBAC1 cloning vector at the library was cloned in the pTARBAC1 cloning vector at the "note" after using Mbol partially digested male C57BL/6J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 473)
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RPCI-24-397C22.TV RPCI-24 Mus musculus genomic clone
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Indels
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Bos taurus (cow)
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AUTHORS
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                                                                                        Eukaryodia Germatophyta; Embryophyta; Tracheophyta; Spermatophyta; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oooldees; Triticae; Triticum.

1 (bases 1 to 505)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Malo,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea
bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
/mol_type="mRNA"
/do_xref="taxon:4565"
/do_ref="taxon:4565"
/clone="wri.pk0117.c5"
/tissue_type="root"
/clone_lib="warl"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
Xho1; Wheat (Triticum aestivum L.) root; 7 day old
seedling, light grown"
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Oupublished (2001)
Outublished (2001)
Other GSSe: BONP041TR
Contact: Chris Town
                                                                                                                                                                                                                                                                      Crop Genetics
E. I. DuPont de Nemours and Company
Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631.2602
Fax: 302-631-2607
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                         Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GAGGATCTTGTCAGGAGCGATAGGCT 28
                                                       Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                CA610501.1 GI:25165663
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Fax: 301-838-0208
                                                                              Triticum aestivum
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Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Corter. Vector Trimmi g: Cross match from Washington University Genome Center. Vector Trimmi g: This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF046684 BY250020A10B3 Soares normalized bovine placenta Bos taurus cDNA clone BF250020A10B3 5', mRNA sequence.
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/clone_lib="Soares normalized bovine placenta"
/clone=Torgan: placenta; Vector: pT712Pc; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Lewin, H. A. W. Reck Center for Comparative and Functional Genomics W. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
/organism="Brassica oleracea"
/mol type="genomic DNA"
/strān="TO1000DH3"
/db xref="Laxon:3712"
/clone="BONPU41"
/clone="BONPU41"
/clone="BONPU41"
/clone="BONPU41"
/clone="BONPU41"
/clone="Webcor: phoci; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into phoci using BstXI linkers"
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1 (bases 1 to 636)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
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                                                                                                                                                                                                                                                                                                                                   Length 548;
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BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 636 Std Error: 0.00
Plate: BP250020A10 row: B column: 3
Seq primer: ACCGGATAACAATTCACACAGGA
High quality sequence stop: 636.
Location/Qualifiers
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/db_xref="taxon:9913"
/clone="BP250020A10B3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
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Unpublished (2000)
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/USE / ACT | The Control of the Cont
                                                                                                                                                                                                                                                             Contact: Majib M. El-Sayed
Contact: Majib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through Research Genetics, Alabama, USA. Sheared DNA
end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Reverse
Class: shotgun.
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                                                L (Dases I to /11)
El-Sayed,N., Zhao,Al., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
Unpublished (1999)
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/organism="Trypanosoma brucei"
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Hypocrea jecorina
Bybaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreacea; Hypocrea.
1 (bases 1 to 63)
Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:51453"
/clone=tric087xj04"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."
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Sheared DNA-57B2.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-57B2, genomic survey sequence.
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                              65.3%; Score 19.6; DB 2; Length 636; larity 84.6%; Pred. No. 6.8e+02; Conservative 0; Mismatches 4; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FERS Microbiol. Lett. 230 (2), 275-282 (2004)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph dean@ncgu.edu
Seq primer: LT-Fl primer.
Location/Qualifiers
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/mol_type="mRNA"
/strain="QM6a"
                                                                                                                                                                                   165 TCGAGGATCTTGTCAGGCATGGTAGG 140
                                                                                                                                                     5 GGATCTTGTCAGGAGCGATAGGCTGC 30
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Query Match
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BOHUXSJTR BO 2 3 KB Brassica oleracea genomic clone BOHUX53, BH687374
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BOGGW35TF BOGQ Brassica oleracea genomic clone BOGGW35, genomic
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 812)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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/note="Vector: pHOS1; Site_1: BstX1; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstX1 linkers"
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Other GSSs: BOGGWASTR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.3%; Score 19.6; DB 8; Length 772; ilarity 84.6%; Pred. No. 7e+02; Conservative 0; Mismatches 4; Indels (
  Query Match 65.3%; Score 19.6; DB 7; Length 753; Best Local Similarity 84.6%; Pred. No. 7e+02; Matches 22; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cdtown@tigr.org
DNA is from a_doubled haploid provided by Tom Osborn.
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Class: sheared ends.
Location/Qualifiers
1. 772
/organism="Brassica oleracea"
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Fax: 301-838-0208
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Hypocrea jecorina cDNA clone tric034xf13, mRNA sequence.
CF873769
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Hypocrea jecorina
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreacea; Hypocrea.
1 (bases 1 to 753)
Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:51453"
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/note="Vector: pREB3Y; Site_1: Not I/Sal 1; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."
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Pred. No. 7e+02;
0; Mismatches 4; Indels (
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Contact: Ralph A. Dean
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0020
Email: ralph Gean@ncsu.edu
Seq primer: LT-Fl primer.
Location/Qualifiers
Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
927 Pate: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Seq primer: LT-F1 primer.
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/strain="QM6a"
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/mol_type="mRNA"
/strain="QM6a"
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1 Similarity 84.6%;
22; Conservative (
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p DNA linear GSS 13-JUL-2004 propinguum genomic clone
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD

clade, Panicoideae, Andropogoneae, Sorghum.

(bases 1 to 318)

Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Kudrna, D.,

Muller, C., Soderlund, C., Bowers, J.E., Paterson, A.H. and Wing, R.

Physical mapping of the sorghum genome

Unpublished (2004)
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ab35d07.s1 Stratagene HeLa cell s3 937216 Homo sapiens CDNA clone
IMAGE:842797 3' similar to gb:S71381 PROTEASOME BETA CHAIN
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/clone="SP_Ba0072B17"
/note="Wetcor: pBeloBAC11; Site 1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)
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                                                                  Length 823;
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Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 629 595
Fax: 520 621 1259
Email: http://genome.arizona.edu
and Nitrogen sources and concentrations."
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64.7%; Score 19.4; DB 9;
Best Local Similarity 79.3%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 6;
                                                               ch 65.3%; Score 19.6; DB 6; 25; Similarity 84.6%; Pred. No. 7.1e+02; 22; Conservative 0; Mismatches 4;
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0072 row: B column: 17
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
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Hypocrea jecorina
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreace; Hypocrea.
1 (bases 1 to 823)
Foreman, P.K., Brown, D.B., Dankmeyer, L., Dean, R., Diener, S.,
Dunn-Colleman, N.S., Goedegbuur, F., Houfek, T.D., England, G.J.,
Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,
Olivares, H.A., Teunissen, P.J., Yao, J. and Ward, M.
                                                                                                                                                                                                                                                                                             / . . 812
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/ strain="1701000DH3"
/ db_xref="taxon:3712"
/ clone="BOHUX53"
/ clone="1b="802" 3 KB"
/ note="vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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                                                                                                                                      Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Dana is crom a doubled haploid provided by Tom Osborn.
Seg primer: TR
Class: sheared ends.
Location/Qualifiers
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  Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA
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Genencor Intl.
Genencor Intl.
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-Fl primer.
Location/Qualifiers
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J. Biol. Chem. 278 (34), 31988-31997 (2003)
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                                               Other GSSs: BOHUX53TF
Contact: Chris Town
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Gaps

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AMCNUNC.NRHW1-00311-E12-A W rat hypo-pit (10478) Rattus norvegicus CB773582. GI:29861973
EST.73582. GI:29861973
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AJ706082 BLPD01 Homo sapiens cDNA clone BLPD01229, mRNA sequence.
AJ706082
AJ706082.1 GI:49472081
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Corganism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="nrival-00311-e12"

/clone="nrival-00311-e12"

/clone="nrival-00311-e12"

/clone="nrival-0041-e12"

/clone="nrival-0041-e12"

/clone="vector: pSPORT1; Site_1: Sal1; Site_2: Not1; W rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                 /db_xref="taxon:9615"
/clone_lib="hog Library"
/note="81te_l: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 417-4881
Plate: 00311 row: e column: 12.
Location/Qualifiers
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64.7%; Score 19.4; DB 6; Length 395;
Best Local Similarity 79.3%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 6; Indels
                                                                                                                        /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                383 rccaddarcardccccdadccaaadcrid 355
                                                                                                                                                                                                                                                                                                                                                                                        1 TCGAGGATCTTGTCAGGAGCGATAGGCTG 29
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                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 395)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
  Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                              Best Local Similarity 79.3
Matches 23; Conservative
                                                                                                         1. .390
                                                               Class: shotgun.
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AJ706082
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Enkaryota; Merazoa; Chordata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 328)

RS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lenno,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1800

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1065 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tigr-gss-dog-17000332602409 Dog Library Canis familiaris genomic genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo gapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:842797"
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Canis familiaris
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Best Local Similarity
Matches 23; Conserv
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CE837920/c
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/worganisma."Trypanosoma brucei"
/wol_type="genomic DNA"
/strain="Trypanosoma brucei"
/db_txref="texton:5691"
/clone="lib="Sheared DNA-17N21"
/clone="lib="Sheared DNA-17N21"
/clone="lib="Sheared DNA-17N21"
/clone="lib="Sheared DNA"
/note="vector: pUC18; Site 1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shocgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma.

Trypanosoma.

Is (bases 1 to 555)

El-Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerzard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Donelson, J., Fraser, C. and Adams, M.

Donelson, J., Fraser, C. and Adams, M.

Unpublished (1999)

Other GSSs: Sheared DNA library

Unpublished (1999)

Other GSSs: Sheared DNA-17N21.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                     AQ652667 linear GSS 22-JUN-1999
Sheared DNA-17N21.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-17N21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
       /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
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Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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                                                                                                    64.7%; Score 19.4; DB 9; Length 466; 79.3%; Pred. No. 8e+02; ive 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                  2 CGAGGATCTTGTCAGGAGCGATAGGCTGC 30
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AQ652667.1 GI:5145853
                                                                           Query Match
Best Local Similarity 79.39,
Thes 23; Conservative
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AQ652667/c
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Sucaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

I (bases 1 to 466)

S Kim,H.; Yu,Y.; Wissotski,M.; Yost,D.; Stum,D.; Rao,K.; Kudrna,D.;

Muller,C., Soderlund,C., Bowers,J.E.; Paterson,A.H. and Wing,R.

Physical mapping of the sorghum genome

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 625 9595

Fax: 520 621 1259

Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL702561
SP Ba0085N23.f SP Ba Sorghum propinguum genomic clone SP Ba0085N23.f SP Concere SP Ba0085N23 5', genomic survey sequence.
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                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 424)

DePitta,C., Tombolan,L., Kronnie,G., Romualdi,C., Vitulo,N., Basso,G. and Lanfranchi,G.
A leukemia-enriched onNA microarray platform identified new transcripts with relevance to the biology of leukemias

Contact: DePitta C

Biology and CRIBI
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/mol type="grononic DNA"
/db_xref="taxon:132711"
/clone="SP_Ba0085N23"
/clone_lib="SP_Ba"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC AC CCA
Plate: OBS row: N column: 23
Seg primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="bone marrow"
/clone_lib="BLPD01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 rcgaggrrcrrcrgaggacgargcrg 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TCGAGGATCTTGTCAGGAGCGATAGGCTG 29
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                            Via U. Bassi, 58/B, 35131, ITALY.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BLPD01229"
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/note="caucasian"
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                                                                                                                                                                                                                                                                                                                     University of Padova
  EST.
Homo sapiens (human)
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Sorghum propinguum
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                                                       sapiens
                                                       Homo
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1. .616 "Organism="Metarhizium anisopliae" |
/mol type="mRNA" |
/fucl type="mRNA" |
/fucl type="mRNA" |
/fucl xref="taxon:5530" |
/clone="M##1803" |
/clone="m##1803"
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AJZ74168 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae
AJZ74168
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Screen, S.E., Mathur, P. and St. Leger, R.J.
EST analysis of the insect pathogenic fungus Metarhizium anisopliae
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ed0005D08f"
/tissue_type="Pibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | jab host="E. coli"
|clone lib="Gossypium arboreum 7-10 dpa fiber library"
|note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
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Metarhizium anisopliae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
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4112 Plant Sciences Building, College Park, MD 20742, USA.
Location/Qualifiers
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Contact: Wing RA
Clemson University Genomics Institute
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Fax: 864 656 4293
Total High Quality bases = 322
Seg primer: TANTACACTCACTATACGG
High quality sequence start: 13
High quality sequence stop: 546.
Location/Qualifiers
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/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
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dpa fiber library Gossypium
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Wing,R.A., Frisch,D., Yu.Y., Main,D., Rambo,T., Simmons,J.,
Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
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1 (bases 1 to 594)

1 (bases 2 to 594)

1 (bases 3 to 594)

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/clone=lib="SP_Ba"
/note="Wetcor: _DBeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
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Porbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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/organism="Sorghum propinguum"
/mol tvne="genomic DNA"
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0065 row: A column: 04
Seq primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
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Sorghum propinguum
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BQ401535/c
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Sorghum propinguum
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panticoideae; Andropogoneae; Sorghum.

(Dases 1 to 627)

Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Kudrna,D.,
Kim,H., Yu,Y., Missotski,M., Yost,D., Stum,D., Rao,K., Kudrna,D.,
Physical mapping of the sorghum genome
Unpublished (2004)
                                                                                                                              1...621

/organism="Cucumis sativus"

/mol_type="makNa"

/mol_type="makNa"

/db_xref="taxon:3659"

/sex="monoecious"

/clone_lib="Cucumber leaf"

/note="Vector: pAD-GAL4; Site_1: EcoRI; Site_2: XhoI"
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Mmol type="genomic DNA"
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/clone="SP_Ba009F13"
/note="Wetcor: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fel: 520 626 9595
Fax: 520 621 1259
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64.7%; Score 19.4; DB 9;
Best Local Similarity 79.3%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                         Query Match

64.7%; Score 19.4; DB 7;

Best Local Similarity 79.3%; Pred. No. 8.4e+02;

Matches 23; Conservative 0; Mismatches 6;
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0095 row: F column: 13
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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MI 48824, USA
Tel: 517 353 0890
Fax: 517 355 5191 x431
Email: grumet@mnsu.edu
Plate: RG11 row: F column: 05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: http://genome.arizona.edu
PCR PRimers
                                                                                                            Location/Qualifiers
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CL703342.1 GI:50269617
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CL703342
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                                                                                                                                                     BZ519836 620 bp DNA linear GSS 16-DEC-2002 BOMQD55TF BO_2_3_KB Brassica oleracea genomic clone BOMQD55, genomic survey sequence.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Cucurbitales, Cucurbitaceae, Cucumis.
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Rebecca Grumet
Michigan State University
Horticulture Department, Michigan State University, East Lansing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 621)
Grumet, R. and McGrath, M.
Development of genomic tools for cucumber (Cucumis sativus L.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /_organism="Brassica oleracea"
/mol type="genomic DNA"
/mol type="genomic DNA"
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/clone="BOWQD55"
/clone="BOWQD55"
/note="bowcor: pHGS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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Cother GSSs: BOMODSTR
Contact: Chris Town
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RG11 F05 Cucumber leaf Cucumis sativus cDNA, mRNA sequence.
CKO8<u>6</u>094
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Emails cdtown@tigr.org
Seg primer: TF
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                                    515 TCGAGGATATAGTCGGAAGCGGGAGGCTG 487
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  1 TCGAGGATCTTGTCAGGAGCGATAGGCTG 29
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                           Brassica oleracea
                                                                                                                                                                                                                          BZ519836
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VERSION
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BZ519836/c
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AUTHORS
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CK086094
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E 1 (bases 1 to 636)

S Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,

Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,

Katzenburger, F., King, L., Miller, B., Muller, S., Naschmero, L.,

Zutavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.

Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)

Longublished (2002)

Longublished (2002)

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884

Email: mccombie@cshl.org

Plate: hv86 row: c column: 01

Seq primer: -21Mi3UnivFwd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BZ329488 636 bp DNA linear GSS 06-NOV-2002 hv86c01.bl WGS-Sbicolorf (JM107 adapted methyl filtered) Sorghum bicolor genomic clone hv86c01 5', genomic survey sequence.
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Sorghum bicolor
Sorghum bicolor
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                          /clone="zmwBwa0537J20"
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 634;
                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Emall: whitelaw@tigr.org
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.7%; Score 19.4; DB 9;
79.3%; Pred. No. 8.4e+02;
ive 0; Mismatches 6;
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/organism="Zea mays"
/mol_type="genomic DNA"
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Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 79.5.
Thes 23; Conservative
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                                                                                                                                                                                                                    Seq primer: TF
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BZ329488/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chour, Tsurumi -Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp), URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                          AG125336 633 bp DNA linear GSS 04-NOV-200
Pan troglodytes DNA, clone: PTB-135124.R, genomic survey sequence.
AG125336
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 64.7%; Score 19.4; DB 9; Length 633; Similarity 79.3%; Pred. No. 8.4e+02; 23; Conservative 0; Mismatches 6; Indels
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/db_xref="taxon:9598"
/clone="PTB-135I24.R"
       173 CGACTATCTTTCAGGATCAATTGGCTGC 201
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Pan troglodytes
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R.Site 2 : SacI
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CC688069/c
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AG125336/c
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Tel: 301-838-5843
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tigr-gase-dog-17000331469523 Dog Library Canis familiaris genomic, genomic survey sequence.
end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, b/g reads in DUC19). The same ligation was transformed in either JM107 or BH5a."
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OGVEGOSTV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0537J21,
QENOMIC SULVEY SEQUENCE.
CC732980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
I (bases I to 668)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:9615"
/clone lib="Dog Library"
/note="Site l: BstXI; Libraries were prepared from
peripheral blood"
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                                                                                                                    64.7%; Score 19.4; DB 8; Length 636; larity 79.3%; Pred. No. 8.4e+02; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                           309 CGACTATCTTTCAGGACCAATTGGCTGC 281
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/strain="Standard Poodle"
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                                                                                                                                                                                                                                                                                                                                                                                 CE805733.1 GI:37146655
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                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (dog)
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les 23; Conserv
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Best Local 8
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CC732980/c
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CE805733/c
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SP_Ba0010H14.r SP_Ba Sorghum propinguum genomic clone SP_Ba0010H14 3', genomic survey sequence.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
1 (bases 1 to 699)
Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Kudrna, D.,
Muller, C., Soderlund, C., Bowers, J.E., Paterson, A.H. and Wing, R.
Physical mapping of the sorghum genome
Unpublished (2004)
                                                                                1 (bases 1 to 679)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Corlek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSS: OGVEOS9TH
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/clone="ZWMBMa053721"
/clone_lib="XM_0.7_1.5_KB"
/note="Yoctor: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic_DNA library"
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Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0010 row: H column: 14
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
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/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                        Contact: Cathy Whitelaw
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Class: sheared ends.
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clone OSJNEc04D10 3', mRNA sequence.
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Contact: Rod A. Wing
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 6295
Fax: 520 621 1259
Email: http://genome.arizona.edu
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Sorghum propinguum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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Corganism="Sorghum propinquum"

/mol_type=genomic DNA"

/db_xrefe="teaxon:132711"

/clone="SP_Ba0064121"

/clone=lib="SP_Ba"

/note="Voctor: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
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| db xref="taxon:13211"
| clone="SP_Ba0010H14"
| clone lib="SP_Ba"
| note="NP_BeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0064 row: L column: 21
Seq primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                         108 CGACTATCTTTCAGGATCAATTGGCTGC 136
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CL700732
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CB653308 710 bp mRNA linear EST 09-APR-2003 OSJNEC04D10.r OSJNEC Oryza sativa (japonica cultivar-group) cDNA

RESULT 40 CB653308/c LOCUS DEFINITION

152 CGAATÁTCTTTTCAGGATCAATTGGCTGC 180

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/tissue_type="Leaf"
/dev_stage="3 week"
/dev_lab_host="bH108"
/clone_llb="OSMBc"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 710)
Jantasuriyarat, C. Lu, G. Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Rudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .710 //organism="Oryza Bativa (japonica cultivar-group)"
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BACKWARD: gga aac agc tat gac cat g
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Fax: 520 621 9288
Email: http://genome.arizona.edu
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Job time : 1796.05 secs
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CB653308.1 GI:29657033
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Best Local Similarity
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